SEQUENCE LISTING

The following Sequence Listing is submitted pursuant to 37 CFR 1.821. A copy in computer readable form is also submitted herewith.

Applicants assert pursuant to 37 CFR 1.821(f) that the content of the paper and computer readable copies of SEQ ID NO:1 through SEQ ID NO:88 submitted herewith are the same.

(1) GENERAL INFORMATION:

(i) APPLICANT: Frank, Glenn R.
Wu Hunter, Shirley
Wallenfels, Lynda

(ii) TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS AND APPARATUS TO COLLECT SUCH PROTEINS

(iii) NUMBER OF SEQUENCES: 88

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: SHERIDAN ROSS P.C.
(B) STREET: 1700 LINCOLN ST., SUITE 3500
(C) CITY: DENVER
(D) STATE: CO
(E) COUNTRY: U.S.A.
(F) ZIP: 80203

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Connell, Gary J.
(B) REGISTRATION NUMBER: 32,020
(C) REFERENCE/DOCKET NUMBER: 2618-17-C4

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 303/863-9700
(B) TELEFAX: 303/863-0223

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Arg Gly Asn His Val Phe Leu Glu Asp Gly Met Ala Asp Met Thr
1 5 10 15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr
20 25

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: Xaa = Tyr or Asp
(B) LOCATION: 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Lys Tyr Arg Asn Xaa Xaa Thr Asn Asp Pro Gln Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Glu Ile Lys Arg Asn Asp Arg Glu Pro Gly Asn Leu Ser Lys Ile Arg
1 5 10 15

Thr Val Met Asp Lys Val Ile Lys Gln Thr Gln
20 25

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: Xaa = Ala or His
(B) LOCATION: 8

(ix) FEATURE:
(A) NAME/KEY: Xaa = Ala or His
(B) LOCATION: 9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Leu Lys Asp Asn Asp Ile Tyr Xaa Xaa Arg Asp Ile Asn Glu Ile Leu
1 5 10 15

Arg Val Leu Asp Pro Ser Lys
20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asn Tyr Gly Arg Val Gln Ile Glu Asp Tyr Thr Xaa Ser Asn His Lys
1 5 10 15

Asp Xaa Glu Glu Lys Asp Gln Ile Asn Gly Leu
20 25

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Lys Tyr Arg Asn Xaa Tyr Thr Asn Asp Pro Gln Leu Lys Leu Leu Asp
1 5 10 15

Glu Gly

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Tyr Phe Asn Asp Gln Ile Lys Ser Val Met Glu Pro Xaa Val Phe Lys
1 5 10 15

Tyr Pro Xaa Ala Xaa Leu
20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..20
(D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TGRTTTCCWA TRAARTCTTC 20

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 225 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAATTCGGCA CGAGTGAAAT TCAATATTTT GTTTTACATT AAATTTTTCA AATTCGATAT 60

GAAATTTTTA CTGGCAATTT GCGTGTTGTG TGTTTTATTA AATCAAGTAT CTATGTCAAA 120

AATGGTCACT GAAAAGTGTA AGTCAGGTGG AAATAATCCA AGTACAGAAG AGGTGTCAAT 180

ACCATCTGGG AAGCTTACTA TTGAAGATTT TTGTATTGGA AATCA 225

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..15
(D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AATTCGGCAC GAGTG 15

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 565 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 45..314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
TGAAATTCAA TATTTTGTTT TACATTAAAT TTTTCAAATT CGAT ATG AAA TTT TTA      56
                                                 Met Lys Phe Leu
                                                   1

CTG GCA ATT TGC GTG TTG TGT GTT TTA TTA AAT CAA GTA TCT ATG TCA      104
Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln Val Ser Met Ser
  5                  10                  15                  20

AAA ATG GTC ACT GAA AAG TGT AAG TCA GGT GGA AAT AAT CCA AGT ACA      152
Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn Asn Pro Ser Thr
                 25                  30                  35
```

```
GAA GAG GTG TCA ATA CCA TCT GGG AAG CTT ACT ATT GAA GAT TTT TGT       200
Glu Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile Glu Asp Phe Cys
            40                  45                  50

ATT GGA AAT CAT CAA AGT TGC AAA ATA TTT TAC AAA AGT CAA TGT GGA       248
Ile Gly Asn His Gln Ser Cys Lys Ile Phe Tyr Lys Ser Gln Cys Gly
        55                  60                  65

TTT GGA GGT GGT GCT TGT GGA AAC GGT GGT TCA ACA CGA CCA AAT CAA       296
Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr Arg Pro Asn Gln
    70                  75                  80

AAA CAC TGT TAT TGC GAA TAACCATATT CCGGATGAAA GACCAAATTG              344
Lys His Cys Tyr Cys Glu
 85                  90

ATATAAATTA CTAAAATTAT GCTAGATAGC AATCATAAAA TTTTGAAGTT TTCAATGATC     404

CTAACATGTT TTGCCTCCAA TTTATTTTAA CAGCAAATTG CTGGAACTTA CCGTACCGTA     464

ACTAAATGTT CAAGAAATAC TGAATGTTTA CAAATAGATT ATTATAAATA TTGTAACATT     524

GTCTAATATT TATAAGAATT ATATAAACTG AATTGCAAAA A                         565
```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
Met Lys Phe Leu Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln
 1               5                  10                  15

Val Ser Met Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn
            20                  25                  30

Asn Pro Ser Thr Glu Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile
        35                  40                  45

Glu Asp Phe Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Tyr Lys
    50                  55                  60

Ser Gln Cys Gly Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr
65                  70                  75                  80

Arg Pro Asn Gln Lys His Cys Tyr Cys Glu
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
ATG AAA TTT TTA CTG GCA ATT TGC GTG TTG TGT GTT TTA TTA AAT CAA        48
Met Lys Phe Leu Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln
  1               5                  10                  15

GTA TCT ATG TCA AAA ATG GTC ACT GAA AAG TGT AAG TCA GGT GGA AAT        96
Val Ser Met Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn
             20                  25                  30

AAT CCA AGT ACA GAA GAG GTG TCA ATA CCA TCT GGG AAG CTT ACT ATT       144
Asn Pro Ser Thr Glu Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile
         35                  40                  45

GAA GAT TTT TGT ATT GGA AAT CAT CAA AGT TGC AAA ATA TTT TAC AAA       192
Glu Asp Phe Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Tyr Lys
     50                  55                  60

AGT CAA TGT GGA TTT GGA GGT GGT GCT TGT GGA AAC GGT GGT TCA ACA       240
Ser Gln Cys Gly Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr
 65                  70                  75                  80

CGA CCA AAT CAA AAA CAC TGT TAT TGC GAA                              270
Arg Pro Asn Gln Lys His Cys Tyr Cys Glu
                 85                  90
```

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
Met Lys Phe Leu Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln
  1               5                  10                  15

Val Ser Met Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn
             20                  25                  30

Asn Pro Ser Thr Glu Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile
         35                  40                  45
```

```
Glu Asp Phe Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Tyr Lys
     50                  55                  60

Ser Gln Cys Gly Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr
 65                  70                  75                  80

Arg Pro Asn Gln Lys His Cys Tyr Cys Glu
                 85                  90
```

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..26
(D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AGTGGATCCG TCAAAAATGG TCACTG 26

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..28
(D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCGGAATTCG GTTATTCGCA ATAACAGT 28

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 897 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 97..568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```
CCGAAATCTC CTATCACAGT GTACGGAGTG TAAAATATTG TTGAAGTATT TTGAAATTTA      60

TTAATTTATT CGAAAAGGAG ATTTCATTAA ATAAAA ATG GTT TAC GAA AGT GAC      114
                                        Met Val Tyr Glu Ser Asp
                                          1               5

TTT TAC ACG ACC CGT CGG CCC TAC AGT CGT CCG GCT TTG TCT TCA TAC      162
Phe Tyr Thr Thr Arg Arg Pro Tyr Ser Arg Pro Ala Leu Ser Ser Tyr
            10                  15                  20

TCC GTA ACG GCA CGT CCA GAG CCG GTT CCT TGG GAC AAA TTG CCG TTC      210
Ser Val Thr Ala Arg Pro Glu Pro Val Pro Trp Asp Lys Leu Pro Phe
        25                  30                  35

GTC CCC CGT CCA AGT TTG GTA GCA GAT CCC ATA ACA GCA TTT TGC AAG      258
Val Pro Arg Pro Ser Leu Val Ala Asp Pro Ile Thr Ala Phe Cys Lys
    40                  45                  50

CGA AAA CCT CGC CGA GAA GAA GTT GTT CAA AAA GAG TCC ATT GTT CGA      306
Arg Lys Pro Arg Arg Glu Glu Val Val Gln Lys Glu Ser Ile Val Arg
55                  60                  65                  70

AGG ATC AAT TCT GCA GGA ATT AAA CCC AGC CAG AGA GTT TTA TCG GCT      354
Arg Ile Asn Ser Ala Gly Ile Lys Pro Ser Gln Arg Val Leu Ser Ala
                75                  80                  85

CCA ATA AGA GAA TAC GAA TCC CCA AGG GAC CAG ACC AGG CGT AAA GTT      402
Pro Ile Arg Glu Tyr Glu Ser Pro Arg Asp Gln Thr Arg Arg Lys Val
            90                  95                  100

TTG GAA AGC GTC AGA AGA CAA GAA GCT TTT CTG AAC CAA GGA GGA ATT      450
Leu Glu Ser Val Arg Arg Gln Glu Ala Phe Leu Asn Gln Gly Gly Ile
        105                 110                 115

TGT CCA TTG ACC ACC AGA AAT GAT GAC ATG GAT AGA CTT CTA CCC CGT      498
Cys Pro Leu Thr Thr Arg Asn Asp Asp Met Asp Arg Leu Leu Pro Arg
    120                 125                 130

CTC CAC AGT TCA CAC ACA ACA CCT TCT GCG GAT AGG AAA GTT TTG TTG      546
Leu His Ser Ser His Thr Thr Pro Ser Ala Asp Arg Lys Val Leu Leu
135                 140                 145                 150

ACC ACT TTT CAC AGA AGA TAC T GATTAAAAAT GAAAGTTAAG AAATTTGTTG      598
Thr Thr Phe His Arg Arg Tyr
                155

AAGTCATGTG GTGTTTTTTA TACATTCTTT ATTAATCGAT ATTCCTAACG AACGATACGA   658

TAACTTTCGA TAACTTTTTC TGGTTAATTT TGACAAAATA TGCATTTGCA AGCATAACAT   718
```

TCATTTTCAA GGCAAACGCT TTCTGATGAT TATCTTGTTA AAAGTGTGGA AACAAGCGTA 778

GTGTTAACAA ATGCATTGCT TGTTTTGATT ATTTATTTAT CTATTATATA TTCCATATTG 838

TATTGTAGGT GGTGTACTTG GTATTACTAA TACACGTACT TTGTGAAAAA AAAAAAAAA 897

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 157 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Val Tyr Glu Ser Asp Phe Tyr Thr Thr Arg Arg Pro Tyr Ser Arg
1 5 10 15

Pro Ala Leu Ser Ser Tyr Ser Val Thr Ala Arg Pro Glu Pro Val Pro
20 25 30

Trp Asp Lys Leu Pro Phe Val Pro Arg Pro Ser Leu Val Ala Asp Pro
35 40 45

Ile Thr Ala Phe Cys Lys Arg Lys Pro Arg Arg Glu Glu Val Val Gln
50 55 60

Lys Glu Ser Ile Val Arg Arg Ile Asn Ser Ala Gly Ile Lys Pro Ser
65 70 75 80

Gln Arg Val Leu Ser Ala Pro Ile Arg Glu Tyr Glu Ser Pro Arg Asp
85 90 95

Gln Thr Arg Arg Lys Val Leu Glu Ser Val Arg Arg Gln Glu Ala Phe
100 105 110

Leu Asn Gln Gly Gly Ile Cys Pro Leu Thr Thr Arg Asn Asp Asp Met
115 120 125

Asp Arg Leu Leu Pro Arg Leu His Ser Ser His Thr Thr Pro Ser Ala
130 135 140

Asp Arg Lys Val Leu Leu Thr Thr Phe His Arg Arg Tyr
145 150 155

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 471 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
ATGGTTTACG AAAGTGACTT TTACACGACC CGTCGGCCCT ACAGTCGTCC GGCTTTGTCT      60

TCATACTCCG TAACGGCACG TCCAGAGCCG GTTCCTTGGG ACAAATTGCC GTTCGTCCCC     120

CGTCCAAGTT TGGTAGCAGA TCCCATAACA GCATTTTGCA AGCGAAAACC TCGCCGAGAA     180

GAAGTTGTTC AAAAAGAGTC CATTGTTCGA AGGATCAATT CTGCAGGAAT TAAACCCAGC     240

CAGAGAGTTT TATCGGCTCC AATAAGAGAA TACGAATCCC CAAGGGACCA GACCAGGCGT     300

AAAGTTTTGG AAAGCGTCAG AAGACAAGAA GCTTTTCTGA ACCAAGGAGG AATTTGTCCA     360

TTGACCACCA GAAATGATGA CATGGATAGA CTTCTACCCC GTCTCCACAG TTCACACACA     420

ACACCTTCTG CGGATAGGAA AGTTTTGTTG ACCACTTTTC ACAGAAGATA C              471
```

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2706 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 5..2706

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
GCGG ATG AAG AGC ATC GAG GCT TAT ACA AAC AGA TAT GAA ATC ATA GCT       49
     Met Lys Ser Ile Glu Ala Tyr Thr Asn Arg Tyr Glu Ile Ile Ala
       1               5                  10                  15


TCT GAA ATA GTT AAT CTT CGA ATG AAA CCA GAT GAT TTT AAT TTA ATA       97
Ser Glu Ile Val Asn Leu Arg Met Lys Pro Asp Asp Phe Asn Leu Ile
                20                  25                  30

AAA GTT ATT GGT CGA GGA GCA TTT GGT GAA GTA CAG TTA GTG CGA CAC      145
Lys Val Ile Gly Arg Gly Ala Phe Gly Glu Val Gln Leu Val Arg His
            35                  40                  45

AAA TCA ACT GCA CAA GTT TTT GCT ATG AAA CGC CTA TCA AAA TTT GAA      193
Lys Ser Thr Ala Gln Val Phe Ala Met Lys Arg Leu Ser Lys Phe Glu
        50                  55                  60

ATG ATT AAG AGA CCA GAC TCT GCA TTT TTT TGG GAA GAA CGT CAT ATA      241
Met Ile Lys Arg Pro Asp Ser Ala Phe Phe Trp Glu Glu Arg His Ile
    65                  70                  75

ATG GCT CAT GCA AAA TCA GAA TGG ATT GTA CAA TTA CAT TTT GCT TTT      289
```

```
Met Ala His Ala Lys Ser Glu Trp Ile Val Gln Leu His Phe Ala Phe
 80                  85                  90                  95

CAA GAT CAA AAA TAT CTT TAT ATG GTC ATG GAT TAT ATG CCG GGG GGT       337
Gln Asp Gln Lys Tyr Leu Tyr Met Val Met Asp Tyr Met Pro Gly Gly
                100                 105                 110

GAC TTG GTG AGT CTT ATG TCC GAT TAT GAA ATT CCA GAA AAA TGG GCA       385
Asp Leu Val Ser Leu Met Ser Asp Tyr Glu Ile Pro Glu Lys Trp Ala
            115                 120                 125

ATG TTC TAT ACA ATG GAA GTG GTG CTA GCA CTT GAT ACA ATT CAC TCC       433
Met Phe Tyr Thr Met Glu Val Val Leu Ala Leu Asp Thr Ile His Ser
        130                 135                 140

ATG GGA TTT GTA CAT CGT GAT GTT AAA CCT GAT AAT ATG CTT CTA GAC       481
Met Gly Phe Val His Arg Asp Val Lys Pro Asp Asn Met Leu Leu Asp
    145                 150                 155

AAA TAT GGT CAT TTA AAG TTA GCT GAC TTT GGA ACC TGT ATG AAA ATG       529
Lys Tyr Gly His Leu Lys Leu Ala Asp Phe Gly Thr Cys Met Lys Met
160                 165                 170                 175

GAT ACA GAT GGT TTG GTA CGT TCT AAT AAT GCT GTT GGA ACG CCT GAT       577
Asp Thr Asp Gly Leu Val Arg Ser Asn Asn Ala Val Gly Thr Pro Asp
                180                 185                 190

TAC ATT TCT CCC GAA GTT TTG CAG TCC CAA GGT GGT GAA GGA GTT TAC       625
Tyr Ile Ser Pro Glu Val Leu Gln Ser Gln Gly Gly Glu Gly Val Tyr
            195                 200                 205

GGT CGT GAA TGC GAT TGG TGG TCT GTG GGA ATT TTT TTG TAT GAA ATG       673
Gly Arg Glu Cys Asp Trp Trp Ser Val Gly Ile Phe Leu Tyr Glu Met
        210                 215                 220

TTA TTT GGA GAA ACA CCT TTT TAT GCA GAC AGT TTG GTT GGA ACT TAC       721
Leu Phe Gly Glu Thr Pro Phe Tyr Ala Asp Ser Leu Val Gly Thr Tyr
    225                 230                 235

AGT AAA ATT ATG GAT CAC AGA AAC TCA TTA ACT TTT CCT CCA GAA GTG       769
Ser Lys Ile Met Asp His Arg Asn Ser Leu Thr Phe Pro Pro Glu Val
240                 245                 250                 255

GAA ATA AGC CAA TAT GCC CGA TCT TTG ATA CAA GGA TTT TTA ACA GAC       817
Glu Ile Ser Gln Tyr Ala Arg Ser Leu Ile Gln Gly Phe Leu Thr Asp
                260                 265                 270

AGA ACA CAG CGT TTA GGC AGA AAT GAA GTG GAA GAA ATT AAA CGA CAT       865
Arg Thr Gln Arg Leu Gly Arg Asn Glu Val Glu Glu Ile Lys Arg His
            275                 280                 285

CCA TTT TTC ATA AAT GAT CAA TGG ACT TTT GAC AAT TTA AGA GAC TCT       913
Pro Phe Phe Ile Asn Asp Gln Trp Thr Phe Asp Asn Leu Arg Asp Ser
        290                 295                 300

GCC CCA CCT GTA GTG CCA GAG CTG AGT GGT GAT GAT GAT ACA AGG AAC       961
Ala Pro Pro Val Val Pro Glu Leu Ser Gly Asp Asp Asp Thr Arg Asn
    305                 310                 315
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```
TTT GAT GAT ATT GAA CGT GAT GAA ACA CCT GAA GAG AAT TTT CCT ATA      1009
Phe Asp Asp Ile Glu Arg Asp Glu Thr Pro Glu Glu Asn Phe Pro Ile
320                 325                 330                 335

CCA AAA ACT TTT GCT GGT AAT CAT CTG CCA TTT GTT GGA TTC ACA TAT      1057
Pro Lys Thr Phe Ala Gly Asn His Leu Pro Phe Val Gly Phe Thr Tyr
                340                 345                 350

AAT GGT GAT TAC CAA TTA TTA ACA AAT GGA GGT GTT AGA AAT AGT GAT      1105
Asn Gly Asp Tyr Gln Leu Leu Thr Asn Gly Gly Val Arg Asn Ser Asp
            355                 360                 365

ATG GTT GAT ACA AAA TTA AAC AAC ATT TGT GTT TCA AGT AAG GAT GAT      1153
Met Val Asp Thr Lys Leu Asn Asn Ile Cys Val Ser Ser Lys Asp Asp
        370                 375                 380

GTG TTA AAT TTA CAA AAT TTA TTA GAA CAA GAG AAA GGT AAC AGT GAA      1201
Val Leu Asn Leu Gln Asn Leu Leu Glu Gln Glu Lys Gly Asn Ser Glu
    385                 390                 395

AAT TTG AAA ACA AAC ACC CAA TTA TTA AGT AAT AAA TTA GAT GAA CTA      1249
Asn Leu Lys Thr Asn Thr Gln Leu Leu Ser Asn Lys Leu Asp Glu Leu
400                 405                 410                 415

GGT CAG AGA GAA TGT GAA TTA AGG AAT CAG GCT GGA GAT TAT GAG AAA      1297
Gly Gln Arg Glu Cys Glu Leu Arg Asn Gln Ala Gly Asp Tyr Glu Lys
                420                 425                 430

GAA TTG ACT AAA TTC AAA TTA TCG TGC AAA GAA TTA CAA CGT AAG GCA      1345
Glu Leu Thr Lys Phe Lys Leu Ser Cys Lys Glu Leu Gln Arg Lys Ala
            435                 440                 445

GAA TTT GAG AAT GAA TTA CGG CGT AAA ACT GAG TCC TTA CTA GTT GAA      1393
Glu Phe Glu Asn Glu Leu Arg Arg Lys Thr Glu Ser Leu Leu Val Glu
        450                 455                 460

ACA AAG AAA AGA CTA GAC GAA GAG CAG AAT AAA AGA ACT AGA GAA ATG      1441
Thr Lys Lys Arg Leu Asp Glu Glu Gln Asn Lys Arg Thr Arg Glu Met
    465                 470                 475

AAT AAT AAT CAA CAG CAC AAT GAC AAA ATA AAT ATG TTA GAA AAA CAA      1489
Asn Asn Asn Gln Gln His Asn Asp Lys Ile Asn Met Leu Glu Lys Gln
480                 485                 490                 495

ATT AAT GAT TTA CAA GAA AAA TTG AAA GGT GAA TTA GAG CAC AAT CAG      1537
Ile Asn Asp Leu Gln Glu Lys Leu Lys Gly Glu Leu Glu His Asn Gln
                500                 505                 510

AAA TTA AAG AAG CAA GCT GTT GAG CTT AGA GTT GCT CAG TCT GCT ACT      1585
Lys Leu Lys Lys Gln Ala Val Glu Leu Arg Val Ala Gln Ser Ala Thr
            515                 520                 525

GAA CAA CTG AAT AAT GAA TTA CAG GAA ACT ATG CAG GGT TTA CAA ACA      1633
Glu Gln Leu Asn Asn Glu Leu Gln Glu Thr Met Gln Gly Leu Gln Thr
        530                 535                 540

CAA AGA GAT GCT TTA CAA CAA GAA GTA GCA TCT CTC CAA GGC AAA CTT      1681
Gln Arg Asp Ala Leu Gln Gln Glu Val Ala Ser Leu Gln Gly Lys Leu
    545                 550                 555
```

```
TCT CAA GAG AGG AGC TCT AGA TCA CAG GCT TCT GAT ATG CAG ATA GAA      1729
Ser Gln Glu Arg Ser Ser Arg Ser Gln Ala Ser Asp Met Gln Ile Glu
560                 565                 570                 575

CTA GAA GCA AAA TTG CAG GCT CTC CAT ATT GAA CTG GAG CAT GTC AGA      1777
Leu Glu Ala Lys Leu Gln Ala Leu His Ile Glu Leu Glu His Val Arg
                580                 585                 590

AAT TGT GAA GAC AAA GTT ACC CAA GAC AAC AGA CAA CTA TTG GAA AGG      1825
Asn Cys Glu Asp Lys Val Thr Gln Asp Asn Arg Gln Leu Leu Glu Arg
            595                 600                 605

ATA TCA ACA TTG GAG AAA GAA TGT GCT TCT CTA GAA TTA GAA TTG AAA      1873
Ile Ser Thr Leu Glu Lys Glu Cys Ala Ser Leu Glu Leu Glu Leu Lys
        610                 615                 620

GCA ACA CAA AAC AAA TAT GAG CAA GAG GTC AAA GCA CAT CGC GAA ACT      1921
Ala Thr Gln Asn Lys Tyr Glu Gln Glu Val Lys Ala His Arg Glu Thr
    625                 630                 635

GAA AAA TCA AGA CTG GTC AGT AAA GAA GAA GCA AAT ATG GAG GAA GTT      1969
Glu Lys Ser Arg Leu Val Ser Lys Glu Glu Ala Asn Met Glu Glu Val
640                 645                 650                 655

AAA GCA CTC CAA ATA AAA TTA AAT GAA GAG AAA TCT GCT CGA CAG AAA      2017
Lys Ala Leu Gln Ile Lys Leu Asn Glu Glu Lys Ser Ala Arg Gln Lys
                660                 665                 670

TCT GAT CAG AAT TCT CAA GAA AAG GAA CGA CAA ATT TCT ATG TTA TCT      2065
Ser Asp Gln Asn Ser Gln Glu Lys Glu Arg Gln Ile Ser Met Leu Ser
            675                 680                 685

GTG GAT TAT CGT CAA ATC CAA CAG CGT TTG CAA AAG CTA GAA GGA GAA      2113
Val Asp Tyr Arg Gln Ile Gln Gln Arg Leu Gln Lys Leu Glu Gly Glu
        690                 695                 700

TAT AGG CAA GAG AGT GAA AAA GTT AAA GCT CTC CAC AGT CAG ATT GAG      2161
Tyr Arg Gln Glu Ser Glu Lys Val Lys Ala Leu His Ser Gln Ile Glu
    705                 710                 715

CAA GAG CAA CTA AAA AAA TCA CAA TTA CAA AGC GAA TTG GGT GTT CAA      2209
Gln Glu Gln Leu Lys Lys Ser Gln Leu Gln Ser Glu Leu Gly Val Gln
720                 725                 730                 735

AGG TCT CAG ACT GCA CAT TTA ACA GCC AGG GAA GCT CAG CTA GTT GGA      2257
Arg Ser Gln Thr Ala His Leu Thr Ala Arg Glu Ala Gln Leu Val Gly
                740                 745                 750

GAA GTT GCT CAT CTT AGA GAT GCT AAA AGA AAT GTT GAA GAA GAG TTA      2305
Glu Val Ala His Leu Arg Asp Ala Lys Arg Asn Val Glu Glu Glu Leu
            755                 760                 765

CAC AAG TTA AAA ACT GCT CGA TCA GTG GAT AAT GCT CAG ATG AAA GAG      2353
His Lys Leu Lys Thr Ala Arg Ser Val Asp Asn Ala Gln Met Lys Glu
        770                 775                 780

CTT CAA GAA CAA GTT GAA GCC GAG CAA GTT TTC TCG ACT CTT TAT AAA      2401
Leu Gln Glu Gln Val Glu Ala Glu Gln Val Phe Ser Thr Leu Tyr Lys
```

```
    785                 790                 795

ACA CAT TCT AAT GAA CTT AAG GAA GAA CTT GAG GAA AAA TCT CGT CAT      2449
Thr His Ser Asn Glu Leu Lys Glu Glu Leu Glu Glu Lys Ser Arg His
800                 805                 810                 815

ATT CAA GAA ATG GAA GAA GAA AGA GAA AGT TTG GTT CAT CAG CTA CAA      2497
Ile Gln Glu Met Glu Glu Glu Arg Glu Ser Leu Val His Gln Leu Gln
                820                 825                 830

ATT GCA TTA GCT AGA GCT GAT TCA GAG GCA TTG GCG AGA TCA ATA GCT      2545
Ile Ala Leu Ala Arg Ala Asp Ser Glu Ala Leu Ala Arg Ser Ile Ala
            835                 840                 845

GAT GAA AGT ATA GCT GAT TTA GAA AAG GAA AAG ACT ATG AAG GAA TTA      2593
Asp Glu Ser Ile Ala Asp Leu Glu Lys Glu Lys Thr Met Lys Glu Leu
        850                 855                 860

GAA CTA AAA GAA TTA TTA AAC AAA AAT CGT ACT GAA CTT TCC CAG AAA      2641
Glu Leu Lys Glu Leu Leu Asn Lys Asn Arg Thr Glu Leu Ser Gln Lys
    865                 870                 875

GAC ATT TCA ATA AGT GCA TTG CGT GAA CGA GAA AAT GAA CAG AAG AAA      2689
Asp Ile Ser Ile Ser Ala Leu Arg Glu Arg Glu Asn Glu Gln Lys Lys
880                 885                 890                 895

CTT TTA GAA CAA ATC  TC                                             2706
Leu Leu Glu Gln Ile
                900
```

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 900 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```
Met Lys Ser Ile Glu Ala Tyr Thr Asn Arg Tyr Glu Ile Ile Ala Ser
  1               5                  10                  15

Glu Ile Val Asn Leu Arg Met Lys Pro Asp Asp Phe Asn Leu Ile Lys
             20                  25                  30

Val Ile Gly Arg Gly Ala Phe Gly Glu Val Gln Leu Val Arg His Lys
         35                  40                  45

Ser Thr Ala Gln Val Phe Ala Met Lys Arg Leu Ser Lys Phe Glu Met
     50                  55                  60

Ile Lys Arg Pro Asp Ser Ala Phe Phe Trp Glu Glu Arg His Ile Met
 65                  70                  75                  80

Ala His Ala Lys Ser Glu Trp Ile Val Gln Leu His Phe Ala Phe Gln
                 85                  90                  95
```

```
Asp Gln Lys Tyr Leu Tyr Met Val Met Asp Tyr Met Pro Gly Gly Asp
            100                 105                 110

Leu Val Ser Leu Met Ser Asp Tyr Glu Ile Pro Glu Lys Trp Ala Met
        115                 120                 125

Phe Tyr Thr Met Glu Val Val Leu Ala Leu Asp Thr Ile His Ser Met
    130                 135                 140

Gly Phe Val His Arg Asp Val Lys Pro Asp Asn Met Leu Leu Asp Lys
145                 150                 155                 160

Tyr Gly His Leu Lys Leu Ala Asp Phe Gly Thr Cys Met Lys Met Asp
                165                 170                 175

Thr Asp Gly Leu Val Arg Ser Asn Asn Ala Val Gly Thr Pro Asp Tyr
            180                 185                 190

Ile Ser Pro Glu Val Leu Gln Ser Gln Gly Gly Glu Gly Val Tyr Gly
        195                 200                 205

Arg Glu Cys Asp Trp Trp Ser Val Gly Ile Phe Leu Tyr Glu Met Leu
    210                 215                 220

Phe Gly Glu Thr Pro Phe Tyr Ala Asp Ser Leu Val Gly Thr Tyr Ser
225                 230                 235                 240

Lys Ile Met Asp His Arg Asn Ser Leu Thr Phe Pro Pro Glu Val Glu
                245                 250                 255

Ile Ser Gln Tyr Ala Arg Ser Leu Ile Gln Gly Phe Leu Thr Asp Arg
            260                 265                 270

Thr Gln Arg Leu Gly Arg Asn Glu Val Glu Glu Ile Lys Arg His Pro
        275                 280                 285

Phe Phe Ile Asn Asp Gln Trp Thr Phe Asp Asn Leu Arg Asp Ser Ala
    290                 295                 300

Pro Pro Val Val Pro Glu Leu Ser Gly Asp Asp Asp Thr Arg Asn Phe
305                 310                 315                 320

Asp Asp Ile Glu Arg Asp Glu Thr Pro Glu Glu Asn Phe Pro Ile Pro
                325                 330                 335

Lys Thr Phe Ala Gly Asn His Leu Pro Phe Val Gly Phe Thr Tyr Asn
            340                 345                 350

Gly Asp Tyr Gln Leu Leu Thr Asn Gly Gly Val Arg Asn Ser Asp Met
        355                 360                 365

Val Asp Thr Lys Leu Asn Asn Ile Cys Val Ser Ser Lys Asp Asp Val
    370                 375                 380

Leu Asn Leu Gln Asn Leu Leu Glu Gln Glu Lys Gly Asn Ser Glu Asn
385                 390                 395                 400

Leu Lys Thr Asn Thr Gln Leu Leu Ser Asn Lys Leu Asp Glu Leu Gly
```

405 410 415

Gln Arg Glu Cys Glu Leu Arg Asn Gln Ala Gly Asp Tyr Glu Lys Glu
420 425 430

Leu Thr Lys Phe Lys Leu Ser Cys Lys Glu Leu Gln Arg Lys Ala Glu
435 440 445

Phe Glu Asn Glu Leu Arg Arg Lys Thr Glu Ser Leu Leu Val Glu Thr
450 455 460

Lys Lys Arg Leu Asp Glu Glu Gln Asn Lys Arg Thr Arg Glu Met Asn
465 470 475 480

Asn Asn Gln Gln His Asn Asp Lys Ile Asn Met Leu Glu Lys Gln Ile
485 490 495

Asn Asp Leu Gln Glu Lys Leu Lys Gly Glu Leu Glu His Asn Gln Lys
500 505 510

Leu Lys Lys Gln Ala Val Glu Leu Arg Val Ala Gln Ser Ala Thr Glu
515 520 525

Gln Leu Asn Asn Glu Leu Gln Glu Thr Met Gln Gly Leu Gln Thr Gln
530 535 540

Arg Asp Ala Leu Gln Gln Glu Val Ala Ser Leu Gln Gly Lys Leu Ser
545 550 555 560

Gln Glu Arg Ser Ser Arg Ser Gln Ala Ser Asp Met Gln Ile Glu Leu
565 570 575

Glu Ala Lys Leu Gln Ala Leu His Ile Glu Leu Glu His Val Arg Asn
580 585 590

Cys Glu Asp Lys Val Thr Gln Asp Asn Arg Gln Leu Leu Glu Arg Ile
595 600 605

Ser Thr Leu Glu Lys Glu Cys Ala Ser Leu Glu Leu Glu Leu Lys Ala
610 615 620

Thr Gln Asn Lys Tyr Glu Gln Glu Val Lys Ala His Arg Glu Thr Glu
625 630 635 640

Lys Ser Arg Leu Val Ser Lys Glu Glu Ala Asn Met Glu Glu Val Lys
645 650 655

Ala Leu Gln Ile Lys Leu Asn Glu Glu Lys Ser Ala Arg Gln Lys Ser
660 665 670

Asp Gln Asn Ser Gln Glu Lys Glu Arg Gln Ile Ser Met Leu Ser Val
675 680 685

Asp Tyr Arg Gln Ile Gln Gln Arg Leu Gln Lys Leu Glu Gly Glu Tyr
690 695 700

Arg Gln Glu Ser Glu Lys Val Lys Ala Leu His Ser Gln Ile Glu Gln
705 710 715 720

```
Glu Gln Leu Lys Lys Ser Gln Leu Gln Ser Glu Leu Gly Val Gln Arg
                725                 730                 735

Ser Gln Thr Ala His Leu Thr Ala Arg Glu Ala Gln Leu Val Gly Glu
            740                 745                 750

Val Ala His Leu Arg Asp Ala Lys Arg Asn Val Glu Glu Glu Leu His
        755                 760                 765

Lys Leu Lys Thr Ala Arg Ser Val Asp Asn Ala Gln Met Lys Glu Leu
    770                 775                 780


Gln Glu Gln Val Glu Ala Glu Gln Val Phe Ser Thr Leu Tyr Lys Thr
785                 790                 795                 800

His Ser Asn Glu Leu Lys Glu Glu Leu Glu Glu Lys Ser Arg His Ile
                805                 810                 815

Gln Glu Met Glu Glu Glu Arg Glu Ser Leu Val His Gln Leu Gln Ile
            820                 825                 830

Ala Leu Ala Arg Ala Asp Ser Glu Ala Leu Ala Arg Ser Ile Ala Asp
        835                 840                 845

Glu Ser Ile Ala Asp Leu Glu Lys Glu Lys Thr Met Lys Glu Leu Glu
    850                 855                 860

Leu Lys Glu Leu Leu Asn Lys Asn Arg Thr Glu Leu Ser Gln Lys Asp
865                 870                 875                 880

Ile Ser Ile Ser Ala Leu Arg Glu Arg Glu Asn Glu Gln Lys Lys Leu
                885                 890                 895

Leu Glu Gln Ile
            900
```

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 414 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 3..414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```
GA GCT GAT GAG AAT GGA AAT GTG ATT AGC ATT ACT GAT GAA AAT GGA          47
   Ala Asp Glu Asn Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly
    1               5                  10                  15
```

```
AAC ATT ATT AGT ACT ACT GAT GAG AAT GGA AAT GTG ATT AGC ATT ACT        95
Asn Ile Ile Ser Thr Thr Asp Glu Asn Gly Asn Val Ile Ser Ile Thr
                20                  25                  30

GAT GAG AAT GGA AAC ATT ATT AGT ACT ACT GAT GAG AAT GGA AAT GTG       143
Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr Asp Glu Asn Gly Asn Val
            35                  40                  45

ATT AGC ATT ACT GAT GAA AAT GGA AAC ATT ATT AGT ACT ACT GAT GAG       191
Ile Ser Ile Thr Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr Asp Glu
        50                  55                  60

AAT GGA AAT GTG ATT AGC ATT ACT GAT GAG AAT GGA AAT GTG ATT AGC       239
Asn Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly Asn Val Ile Ser
    65                  70                  75

ATT ACT GAT GAA AAT GGA AAC TCG AAT AGC ACT ACT AGT GTT TTC AAT       287

Ile Thr Asp Glu Asn Gly Asn Ser Asn Ser Thr Thr Ser Val Phe Asn
80                  85                  90                  95

GAA ACT GAA AAT ATG ACT GGT GCT GCT GAT ACA AAT GAA TAT TCA ATT       335
Glu Thr Glu Asn Met Thr Gly Ala Ala Asp Thr Asn Glu Tyr Ser Ile
                100                 105                 110

GGT TCT ACT GAC GGA AAT GGA AAT TTT ATA AGT ACT TTT AGT GAT CAT       383
Gly Ser Thr Asp Gly Asn Gly Asn Phe Ile Ser Thr Phe Ser Asp His
            115                 120                 125

GAT TAC GTA AGT AAT ACT GAA GAA AAT GAA  A                            414
Asp Tyr Val Ser Asn Thr Glu Glu Asn Glu
        130                 135
```

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```
Ala Asp Glu Asn Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly Asn
  1               5                  10                  15

Ile Ile Ser Thr Thr Asp Glu Asn Gly Asn Val Ile Ser Ile Thr Asp
            20                  25                  30

Glu Asn Gly Asn Ile Ile Ser Thr Thr Asp Glu Asn Gly Asn Val Ile
        35                  40                  45

Ser Ile Thr Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr Asp Glu Asn
    50                  55                  60

Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly Asn Val Ile Ser Ile
```

```
 65                  70                  75                  80

Thr Asp Glu Asn Gly Asn Ser Asn Ser Thr Thr Ser Val Phe Asn Glu
                85                  90                  95

Thr Glu Asn Met Thr Gly Ala Ala Asp Thr Asn Glu Tyr Ser Ile Gly
            100                 105                 110

Ser Thr Asp Gly Asn Gly Asn Phe Ile Ser Thr Phe Ser Asp His Asp
        115                 120                 125

Tyr Val Ser Asn Thr Glu Glu Asn Glu
    130                 135
```

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 273 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 3..273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```
AT GAG AAT GGA AAT GTG ATT AGC TAT ACT GAT GAA AAT GGA AAC ATT          47
   Glu Asn Gly Asn Val Ile Ser Tyr Thr Asp Glu Asn Gly Asn Ile
     1               5                  10                  15

ATC AGT ACT ACT GAT GAG AAT GGA AAT GTG ATT AGC ATT ACT GAT GAA         95
Ile Ser Thr Thr Asp Glu Asn Gly Asn Val Ile Ser Ile Thr Asp Glu
                20                  25                  30

AAT GGA AAT GTG ATT AGC ATT ACT GAT GAA AAT GGA AAC ATT ATC AGT        143
Asn Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly Asn Ile Ile Ser
            35                  40                  45

ACT ACT GAT GAG AAT GGA AAT GTG ATT AGC ATT ACT GAT GAA AAT GGA        191
Thr Thr Asp Glu Asn Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly
        50                  55                  60

AAT GTG ATT AGC ATT ACT GAT GAA AAT GGA AAC ATT ATT AGT ACT ACT        239
Asn Val Ile Ser Ile Thr Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr
    65                  70                  75

GAT GAG AAT GGA AAT GTG ATT AGC AAT ACT CGA  G                         273
Asp Glu Asn Gly Asn Val Ile Ser Asn Thr Arg
80                  85                  90
```

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```
Glu Asn Gly Asn Val Ile Ser Tyr Thr Asp Glu Asn Gly Asn Ile Ile
 1               5                  10                  15

Ser Thr Thr Asp Glu Asn Gly Asn Val Ile Ser Ile Thr Asp Glu Asn
            20                  25                  30

Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly Asn Ile Ile Ser Thr
        35                  40                  45

Thr Asp Glu Asn Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly Asn
    50                  55                  60

Val Ile Ser Ile Thr Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr Asp
65                  70                  75                  80

Glu Asn Gly Asn Val Ile Ser Asn Thr Arg
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1704 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 24..1406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```
CAGAAACCCG ACATTCTCAA AAT ATG GAA CCT CAA TCG CTG TCT TGG CAA          50
                          Met Glu Pro Gln Ser Leu Ser Trp Gln
                            1               5

CTT CCG ACT CAA GTA GTT CAG CCA GTT TTT GAA CAA CAA ATG CAG ATT        98
Leu Pro Thr Gln Val Val Gln Pro Val Phe Glu Gln Gln Met Gln Ile
 10                  15                  20                  25

CCT GGA TAT AAT ATG CAA ATT CAA TCT AAT TAT TAT CAA ATT CAC CCA       146
Pro Gly Tyr Asn Met Gln Ile Gln Ser Asn Tyr Tyr Gln Ile His Pro
                30                  35                  40

GAA ATG TTG GAT CCA AAT TTG AAC AAT CCT CAG CAG TTA ATG TTT AAT       194
Glu Met Leu Asp Pro Asn Leu Asn Asn Pro Gln Gln Leu Met Phe Asn
```

```
                45                  50                  55

TAT ATG CAA TTA CAA CAA TTG CAG GAA CTA CAA CAT TTA AGT CAA CAA      242
Tyr Met Gln Leu Gln Gln Leu Gln Glu Leu Gln His Leu Ser Gln Gln
        60                  65                  70

CAG CCA ATG CAT CAT GAA TTT GAA CAT CAT ATC CCC ATT CCA CAA GAA      290
Gln Pro Met His His Glu Phe Glu His His Ile Pro Ile Pro Gln Glu
    75                  80                  85

GCA ACT TCA ACT AAT TAC GGT CCA TCC GGA CAG TAT ATT ACT AGT GAC      338
Ala Thr Ser Thr Asn Tyr Gly Pro Ser Gly Gln Tyr Ile Thr Ser Asp
90                  95                  100                 105

GCA ACA TCT TAT CAA TCA ATT GCC CAA CAA TTT GTA CCA CAA CCA CCA      386
Ala Thr Ser Tyr Gln Ser Ile Ala Gln Gln Phe Val Pro Gln Pro Pro
                110                 115                 120

ATT GAA ACT ACC ACC ACG AAA ATA CCT GAA ACT GAA ATT CAA ATT GGC      434
Ile Glu Thr Thr Thr Thr Lys Ile Pro Glu Thr Glu Ile Gln Ile Gly
            125                 130                 135

GTT TCG AAT CAA TAT GCC CAA AAT ATA ACT TAT AAT TCA AAT ATC AGT      482
Val Ser Asn Gln Tyr Ala Gln Asn Ile Thr Tyr Asn Ser Asn Ile Ser
        140                 145                 150

CCT GAA GTG ATT GGA TTC CGA GAA CAT TAT GTT GCG GAA CAG CCT TCT      530
Pro Glu Val Ile Gly Phe Arg Glu His Tyr Val Ala Glu Gln Pro Ser
    155                 160                 165

GGT GAC GTG CTT CAC AAA AGT CAT TTA ACA GAA CAA CCA GCA GAT AAA      578
Gly Asp Val Leu His Lys Ser His Leu Thr Glu Gln Pro Ala Asp Lys
170                 175                 180                 185


AGC ACA CGT GGT GAT CAG GAA CCT GTT AGT GAG ACA GGC TCT GGT TTT      626
Ser Thr Arg Gly Asp Gln Glu Pro Val Ser Glu Thr Gly Ser Gly Phe
                190                 195                 200

TCG TAT GCA CAA ATT TTA TCA CAG GGA CTT AAG CCT ACC CAG CCA TCC      674
Ser Tyr Ala Gln Ile Leu Ser Gln Gly Leu Lys Pro Thr Gln Pro Ser
            205                 210                 215

AAC TCA GTT AAT TTG CTT GCA GAT CGA TCG AGA TCA CCT CTA GAT ACG      722
Asn Ser Val Asn Leu Leu Ala Asp Arg Ser Arg Ser Pro Leu Asp Thr
        220                 225                 230

AAA ACG AAA GAA AAT TAT AAA TCT CCT GGT CGT GTG CAG GAT ATC ACG      770
Lys Thr Lys Glu Asn Tyr Lys Ser Pro Gly Arg Val Gln Asp Ile Thr
    235                 240                 245

AAA ATA ATA GAT GAG AAA CAA AAG TCG TCA AAA GAC ACA GAG TGG CAT      818
Lys Ile Ile Asp Glu Lys Gln Lys Ser Ser Lys Asp Thr Glu Trp His
250                 255                 260                 265

AAT AAG AAA GTG AAA GAA CAT AAA AAA GTG AAA GAT ATC AAA CCT GAT      866
Asn Lys Lys Val Lys Glu His Lys Lys Val Lys Asp Ile Lys Pro Asp
                270                 275                 280
```

```
TTC GAA TCT TCT CAA AGG AAT AAG AAA AGC AAG AAT ATT CCT AAG CAA        914
Phe Glu Ser Ser Gln Arg Asn Lys Lys Ser Lys Asn Ile Pro Lys Gln
            285                 290                 295

ATT GAA AAT ATC ACA CCT CAA CTT GAC AGC TTA CGA TCA CGA GAT ATA        962
Ile Glu Asn Ile Thr Pro Gln Leu Asp Ser Leu Arg Ser Arg Asp Ile
        300                 305                 310

GTA ATT AAG GGA GAA TTA CTA ACA AAA GAT ACT ACA AAA AGT TTA ACT       1010
Val Ile Lys Gly Glu Leu Leu Thr Lys Asp Thr Thr Lys Ser Leu Thr
    315                 320                 325

ACT GTT AAT GTT GAT AGT GAA TTA GAT AGT GTA AAA CCT AAA GAT GAA       1058
Thr Val Asn Val Asp Ser Glu Leu Asp Ser Val Lys Pro Lys Asp Glu
330                 335                 340                 345

AAA CCT GAA CCT TCT GAA CCT AGT AAA ACG TTT ATT GAT ACT TCA GTT       1106
Lys Pro Glu Pro Ser Glu Pro Ser Lys Thr Phe Ile Asp Thr Ser Val
                350                 355                 360

GCA AAG GAT GTT GAT AAT TCT ACA CAG GCG AAC CAT AAA AAG AAG AAA       1154
Ala Lys Asp Val Asp Asn Ser Thr Gln Ala Asn His Lys Lys Lys Lys
            365                 370                 375

AGT AAA TCT AAG CCG AGG AAA ACG GAA CCG GAA GAT GAA ATT GAA AAA       1202
Ser Lys Ser Lys Pro Arg Lys Thr Glu Pro Glu Asp Glu Ile Glu Lys
        380                 385                 390

GCT TTG AAA GAA ATT CAA GCT AGT GAG AAA AAA CTT ACG AAG TCT ATC       1250
Ala Leu Lys Glu Ile Gln Ala Ser Glu Lys Lys Leu Thr Lys Ser Ile
    395                 400                 405

GAT AAC ATT GTG AAT AAA TTT AAT ACA CCA CTT GCT AGT GTT AAA GCC       1298
Asp Asn Ile Val Asn Lys Phe Asn Thr Pro Leu Ala Ser Val Lys Ala
410                 415                 420                 425

GAT GAT TCC AAT TCT ACC AAG GAT AAT GTA CCA GCA AAG AAG AAA AAA       1346
Asp Asp Ser Asn Ser Thr Lys Asp Asn Val Pro Ala Lys Lys Lys Lys
                430                 435                 440

CCT TCG AAG TCA TCT GTT TCT TTA CCT GAG AAT GTA GTA CAA AAT CTA       1394
Pro Ser Lys Ser Ser Val Ser Leu Pro Glu Asn Val Val Gln Asn Leu
            445                 450                 455

TTG ATA CTA ACA TAA CTACTAGTAG CGACAAGATT GAAAACATGC CGCAACCGCA       1449
Leu Ile Leu Thr
        460

ACCAAAAAGA GAAGATTTAC AAGATGCAGC TAAGGAAGTA TTGACTTCAA TAGAGTCAGT     1509

AATGATGCAG TCTGTTGAGA CTATTCCTAT TACGAAGAAA AGAGTAAATA AGAAAAAGAA     1569

TACCACTCAA CAGACGAAGG AATTTGTGGA ACACGAAATA TGCGATACAT CAAAAAATGA     1629

AACTTTAAAA AATATTGAAA AAGAATCGCA TGAGAATATG GCTATATTGC AAACAAGTCC     1689

GAAACCGCCA CTAAG                                                      1704
```

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 461 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```
Met Glu Pro Gln Ser Leu Ser Trp Gln Leu Pro Thr Gln Val Val Gln
 1               5                  10                  15

Pro Val Phe Glu Gln Gln Met Gln Ile Pro Gly Tyr Asn Met Gln Ile
            20                  25                  30

Gln Ser Asn Tyr Tyr Gln Ile His Pro Glu Met Leu Asp Pro Asn Leu
        35                  40                  45

Asn Asn Pro Gln Gln Leu Met Phe Asn Tyr Met Gln Leu Gln Gln Leu
    50                  55                  60

Gln Glu Leu Gln His Leu Ser Gln Gln Gln Pro Met His His Glu Phe
65                  70                  75                  80

Glu His His Ile Pro Ile Pro Gln Glu Ala Thr Ser Thr Asn Tyr Gly
                85                  90                  95

Pro Ser Gly Gln Tyr Ile Thr Ser Asp Ala Thr Ser Tyr Gln Ser Ile
            100                 105                 110

Ala Gln Gln Phe Val Pro Gln Pro Pro Ile Glu Thr Thr Thr Thr Lys
        115                 120                 125

Ile Pro Glu Thr Glu Ile Gln Ile Gly Val Ser Asn Gln Tyr Ala Gln
    130                 135                 140

Asn Ile Thr Tyr Asn Ser Asn Ile Ser Pro Glu Val Ile Gly Phe Arg
145                 150                 155                 160

Glu His Tyr Val Ala Glu Gln Pro Ser Gly Asp Val Leu His Lys Ser
                165                 170                 175

His Leu Thr Glu Gln Pro Ala Asp Lys Ser Thr Arg Gly Asp Gln Glu
            180                 185                 190

Pro Val Ser Glu Thr Gly Ser Gly Phe Ser Tyr Ala Gln Ile Leu Ser
        195                 200                 205

Gln Gly Leu Lys Pro Thr Gln Pro Ser Asn Ser Val Asn Leu Leu Ala
    210                 215                 220

Asp Arg Ser Arg Ser Pro Leu Asp Thr Lys Thr Lys Glu Asn Tyr Lys
225                 230                 235                 240

Ser Pro Gly Arg Val Gln Asp Ile Thr Lys Ile Ile Asp Glu Lys Gln
                245                 250                 255
```

```
Lys Ser Ser Lys Asp Thr Glu Trp His Asn Lys Lys Val Lys Glu His
            260                 265                 270

Lys Lys Val Lys Asp Ile Lys Pro Asp Phe Glu Ser Ser Gln Arg Asn
        275                 280                 285

Lys Lys Ser Lys Asn Ile Pro Lys Gln Ile Glu Asn Ile Thr Pro Gln
    290                 295                 300

Leu Asp Ser Leu Arg Ser Arg Asp Ile Val Ile Lys Gly Glu Leu Leu
305                 310                 315                 320

Thr Lys Asp Thr Thr Lys Ser Leu Thr Thr Val Asn Val Asp Ser Glu
                325                 330                 335

Leu Asp Ser Val Lys Pro Lys Asp Glu Lys Pro Glu Pro Ser Glu Pro
            340                 345                 350

Ser Lys Thr Phe Ile Asp Thr Ser Val Ala Lys Asp Val Asp Asn Ser
        355                 360                 365

Thr Gln Ala Asn His Lys Lys Lys Lys Ser Lys Ser Lys Pro Arg Lys
    370                 375                 380

Thr Glu Pro Glu Asp Glu Ile Glu Lys Ala Leu Lys Glu Ile Gln Ala
385                 390                 395                 400

Ser Glu Lys Lys Leu Thr Lys Ser Ile Asp Asn Ile Val Asn Lys Phe
                405                 410                 415

Asn Thr Pro Leu Ala Ser Val Lys Ala Asp Asp Ser Asn Ser Thr Lys
            420                 425                 430

Asp Asn Val Pro Ala Lys Lys Lys Lys Pro Ser Lys Ser Ser Val Ser
        435                 440                 445

Leu Pro Glu Asn Val Val Gln Asn Leu Leu Ile Leu Thr
    450                 455                 460
```

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1383 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```
ATGGAACCTC AATCGCTGTC TTGGCAACTT CCGACTCAAG TAGTTCAGCC AGTTTTTGAA      60

CAACAAATGC AGATTCCTGG ATATAATATG CAAATTCAAT CTAATTATTA TCAAATTCAC     120

CCAGAAATGT TGGATCCAAA TTTGAACAAT CCTCAGCAGT TAATGTTTAA TTATATGCAA     180
```

TTACAACAAT TGCAGGAACT ACAACATTTA AGTCAACAAC AGCCAATGCA TCATGAATTT 240

GAACATCATA TCCCCATTCC ACAAGAAGCA ACTTCAACTA ATTACGGTCC ATCCGGACAG 300

TATATTACTA GTGACGCAAC ATCTTATCAA TCAATTGCCC AACAATTTGT ACCACAACCA 360

CCAATTGAAA CTACCACCAC GAAAATACCT GAAACTGAAA TTCAAATTGG CGTTTCGAAT 420

CAATATGCCC AAAATATAAC TTATAATTCA AATATCAGTC CTGAAGTGAT TGGATTCCGA 480

GAACATTATG TTGCGGAACA GCCTTCTGGT GACGTGCTTC ACAAAAGTCA TTTAACAGAA 540

CAACCAGCAG ATAAAAGCAC ACGTGGTGAT CAGGAACCTG TTAGTGAGAC AGGCTCTGGT 600

TTTTCGTATG CACAAATTTT ATCACAGGGA CTTAAGCCTA CCCAGCCATC CAACTCAGTT 660

AATTTGCTTG CAGATCGATC GAGATCACCT CTAGATACGA AAACGAAAGA AAATTATAAA 720

TCTCCTGGTC GTGTGCAGGA TATCACGAAA ATAATAGATG AGAAACAAAA GTCGTCAAAA 780

GACACAGAGT GGCATAATAA GAAAGTGAAA GAACATAAAA AAGTGAAAGA TATCAAACCT 840

GATTTCGAAT CTTCTCAAAG GAATAAGAAA AGCAAGAATA TTCCTAAGCA AATTGAAAAT 900

ATCACACCTC AACTTGACAG CTTACGATCA CGAGATATAG TAATTAAGGG AGAATTACTA 960

ACAAAAGATA CTACAAAAAG TTTAACTACT GTTAATGTTG ATAGTGAATT AGATAGTGTA 1020

AAACCTAAAG ATGAAAAACC TGAACCTTCT GAACCTAGTA AAACGTTTAT TGATACTTCA 1080

GTTGCAAAGG ATGTTGATAA TTCTACACAG GCGAACCATA AAAAGAAGAA AAGTAAATCT 1140

AAGCCGAGGA AAACGGAACC GGAAGATGAA ATTGAAAAAG CTTTGAAAGA AATTCAAGCT 1200

AGTGAGAAAA AACTTACGAA GTCTATCGAT AACATTGTGA ATAAATTTAA TACACCACTT 1260

GCTAGTGTTA AAGCCGATGA TTCCAATTCT ACCAAGGATA ATGTACCAGC AAAGAAGAAA 1320

AAACCTTCGA AGTCATCTGT TTCTTTACCT GAGAATGTAG TACAAAATCT ATTGATACTA 1380

ACA 1383

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1758 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1...1758

(ix) FEATURE:

(A) NAME/KEY: W = A or T
(B) LOCATION: 1136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```
CTA GAG ATG GCT AAA TTT CTG ACG GAA ACA TTA GAC GAC ATG ACT CTA          48
Leu Glu Met Ala Lys Phe Leu Thr Glu Thr Leu Asp Asp Met Thr Leu
  1               5                  10                  15

CAA CAC AAA GAT CAC AGA TCA GAA TTG GCT AAA GAG TTT TCA ATT TGG          96
Gln His Lys Asp His Arg Ser Glu Leu Ala Lys Glu Phe Ser Ile Trp
            20                  25                  30

TTT ACG AAA ATG AGA CAG TCT GGC GCT CAA GCC AGT AAC GAA GAA ATC         144
Phe Thr Lys Met Arg Gln Ser Gly Ala Gln Ala Ser Asn Glu Glu Ile
         35                  40                  45

ATG AAA TTT TCA AAA TTG TTT GAA GAT GAA ATC ACT CTT GAC TCG CTG         192
Met Lys Phe Ser Lys Leu Phe Glu Asp Glu Ile Thr Leu Asp Ser Leu
     50                  55                  60

GCG AGG CCG CAA CTT GTT GCT TTG TGC AGG GTA CTA GAA ATC AGT ACT         240
Ala Arg Pro Gln Leu Val Ala Leu Cys Arg Val Leu Glu Ile Ser Thr
 65                  70                  75                  80

TTA GGA ACA ACA AAT TTC TTA AGG TTT CAA CTG CGA ATG AAA CTG CGT         288
Leu Gly Thr Thr Asn Phe Leu Arg Phe Gln Leu Arg Met Lys Leu Arg
                85                  90                  95

TCA TTA GCT GCT GAT GAT AAA ATG ATT CAA AAA GAA GGC ATA GTT TCT         336
Ser Leu Ala Ala Asp Asp Lys Met Ile Gln Lys Glu Gly Ile Val Ser
            100                 105                 110

ATG ACT TAT TCG GAG GTG CAA CAG GCC TGC AGA GCT CGT GGA ATG CGA         384
Met Thr Tyr Ser Glu Val Gln Gln Ala Cys Arg Ala Arg Gly Met Arg
        115                 120                 125

GCT TAT GGT ATG CCT GAA CAT AGG TTG AGG AGG CAA TTG GAA GAC TGG         432
Ala Tyr Gly Met Pro Glu His Arg Leu Arg Arg Gln Leu Glu Asp Trp
    130                 135                 140

ATT AAT TTA AGC TTG AAT GAA AAG GTT CCA CCA TCA TTA TTG CTT TTG         480
Ile Asn Leu Ser Leu Asn Glu Lys Val Pro Pro Ser Leu Leu Leu Leu
145                 150                 155                 160

TCA AGG GCG CTG ATG TTG CCC GAG AAT GTT CCA GTG TCT GAT AAA CTT         528
Ser Arg Ala Leu Met Leu Pro Glu Asn Val Pro Val Ser Asp Lys Leu
                165                 170                 175

AAA GCA ACA ATA AAT GCT CTT CCT GAA ACT ATT GTA ACT CAG ACA AAG         576
Lys Ala Thr Ile Asn Ala Leu Pro Glu Thr Ile Val Thr Gln Thr Lys
            180                 185                 190

GCT GCT ATT GGA GAA AGA GAA GGA AAG ATT GAC AAT AAG ACC AAA ATT         624
Ala Ala Ile Gly Glu Arg Glu Gly Lys Ile Asp Asn Lys Thr Lys Ile
        195                 200                 205

GAG GTC ATC AAA GAG GAA GAA CGC AAA ATT CGC GAA GAG CGC CAA GAA         672
```

```
Glu Val Ile Lys Glu Glu Glu Arg Lys Ile Arg Glu Glu Arg Gln Glu
    210                 215                 220

GCA CGT GAG GAA GAG GAA CAA CGC AAG CAA GCC GAA CTT GCT CTT AAT      720
Ala Arg Glu Glu Glu Glu Gln Arg Lys Gln Ala Glu Leu Ala Leu Asn
225                 230                 235                 240

GCC AGT TCT GCA GCA GCT GAG GCC TCT TCA GCT CAG GAA CTT TTG ATA      768
Ala Ser Ser Ala Ala Ala Glu Ala Ser Ser Ala Gln Glu Leu Leu Ile
                245                 250                 255

GAT ACA GCT CCT GTA ATA GAT GCA GAA AAG ACA CCA AAG GTG GCA ACA      816
Asp Thr Ala Pro Val Ile Asp Ala Glu Lys Thr Pro Lys Val Ala Thr
            260                 265                 270

TCA CCT GTT GAA TCA CCA TTG GCA CCA CCA GAA GTT CTG ATT ATG GGT      864
Ser Pro Val Glu Ser Pro Leu Ala Pro Pro Glu Val Leu Ile Met Gly
        275                 280                 285

GCT CCT AAA ACA CCT GTT GCA ACC GAA GTG GAT AAG AAT GCT GAT GAG      912
Ala Pro Lys Thr Pro Val Ala Thr Glu Val Asp Lys Asn Ala Asp Glu
    290                 295                 300

GTG GAA TTC ACC AAG AAA GAT CTT GAG GTT GTT GAA GAT GCA TTG GAT      960
Val Glu Phe Thr Lys Lys Asp Leu Glu Val Val Glu Asp Ala Leu Asp
305                 310                 315                 320

ACA CTA TCG AAA GAC AAA AAT AAT TTG GTG ATT GAA AAG GAA GTT ATT     1008
Thr Leu Ser Lys Asp Lys Asn Asn Leu Val Ile Glu Lys Glu Val Ile
                325                 330                 335

AAA GAC ATT AAG GAA GAA ATT GCT GAT TAC CAA GAA GAT GTA GAA GAA     1056
Lys Asp Ile Lys Glu Glu Ile Ala Asp Tyr Gln Glu Asp Val Glu Glu
            340                 345                 350

TTG AAA GAA GCC ATA GTT GCT GCT GAG AAA CCA AAG GAT GAG ATA AAA     1104
Leu Lys Glu Ala Ile Val Ala Ala Glu Lys Pro Lys Asp Glu Ile Lys
        355                 360                 365

GAA ACT AAA GGA GCT CAA CGA TTG TTG AAG AWG GTT AAC AAG ATG ATA     1152
Glu Thr Lys Gly Ala Gln Arg Leu Leu Lys Xaa Val Asn Lys Met Ile
    370                 375                 380

ACG AAA ATG GAT ACT GTT GTA CAA GAA ATT GAA AGC AAA GAA TCT GAG     1200
Thr Lys Met Asp Thr Val Val Gln Glu Ile Glu Ser Lys Glu Ser Glu
385                 390                 395                 400

AAG AAA GCC AAA ACA TTG CCA CTT GAA GCT CCT AGG AGC GCT ACT GAA     1248
Lys Lys Ala Lys Thr Leu Pro Leu Glu Ala Pro Arg Ser Ala Thr Glu
                405                 410                 415

ACT CAA GAA TTA GAT GTA AGG AAA GAA AGA GGA GAG ATT TTA ATT GAC     1296
Thr Gln Glu Leu Asp Val Arg Lys Glu Arg Gly Glu Ile Leu Ile Asp
            420                 425                 430

GAA TTA ATG GAC GCT ATT AAG AAA GTT AAA AAT GTG CCA GAC GAA AAT     1344
Glu Leu Met Asp Ala Ile Lys Lys Val Lys Asn Val Pro Asp Glu Asn
        435                 440                 445
```

```
CGC TTG AAA TTA ATT GAG AAC ATT TTG GGC AGG ATC GAT ACT GAC AAA      1392
Arg Leu Lys Leu Ile Glu Asn Ile Leu Gly Arg Ile Asp Thr Asp Lys
    450                 455                 460

GAT AGG CAT ATC AAA GTT GAA GAT GTA TTG AAG GTT ATT GAC ATT GTG      1440
Asp Arg His Ile Lys Val Glu Asp Val Leu Lys Val Ile Asp Ile Val
465                 470                 475                 480

GAA AAA GAA GAT GGT ATC ATG AGT ACA AAA CAA TTA GAT GAG TTG GTT      1488
Glu Lys Glu Asp Gly Ile Met Ser Thr Lys Gln Leu Asp Glu Leu Val
                485                 490                 495

CAG CTT TTG AAA AAG GAG GAA GTT ATT GAA TTG GAA GAA AAG AAA GAA      1536
Gln Leu Leu Lys Lys Glu Glu Val Ile Glu Leu Glu Glu Lys Lys Glu
            500                 505                 510

AAG CAA GAG TCT CAA CAG AAA AGT TTT GTA CCA CCA AGT GAA ACT TTG      1584
Lys Gln Glu Ser Gln Gln Lys Ser Phe Val Pro Pro Ser Glu Thr Leu
        515                 520                 525

CAT CTT GAA TCA TCA CAG CAG AAG AGT ACA GTT CCT AGC TCG GGA CAT      1632
His Leu Glu Ser Ser Gln Gln Lys Ser Thr Val Pro Ser Ser Gly His
    530                 535                 540

GAA GCT AAG GTG TCC GAA GAT GAC TTA AAT GTT AAA AAT AAA AAT TTG      1680
Glu Ala Lys Val Ser Glu Asp Asp Leu Asn Val Lys Asn Lys Asn Leu
545                 550                 555                 560

GAA GAA TCG ACC AAA ACT GAA TGT GGA GCA ATT GAC GAA GAG CAC AGA      1728
Glu Glu Ser Thr Lys Thr Glu Cys Gly Ala Ile Asp Glu Glu His Arg
                565                 570                 575

AGA GAG CAT TGC CAG TAC CCA GAC ATT ACA                              1758
Arg Glu His Cys Gln Tyr Pro Asp Ile Thr
            580                 585
```

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 586 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```
Leu Glu Met Ala Lys Phe Leu Thr Glu Thr Leu Asp Asp Met Thr Leu
  1               5                  10                  15

Gln His Lys Asp His Arg Ser Glu Leu Ala Lys Glu Phe Ser Ile Trp
             20                  25                  30

Phe Thr Lys Met Arg Gln Ser Gly Ala Gln Ala Ser Asn Glu Glu Ile
         35                  40                  45

Met Lys Phe Ser Lys Leu Phe Glu Asp Glu Ile Thr Leu Asp Ser Leu
     50                  55                  60
```

```
Ala Arg Pro Gln Leu Val Ala Leu Cys Arg Val Leu Glu Ile Ser Thr
 65                  70                  75                  80

Leu Gly Thr Thr Asn Phe Leu Arg Phe Gln Leu Arg Met Lys Leu Arg
                85                  90                  95

Ser Leu Ala Ala Asp Asp Lys Met Ile Gln Lys Glu Gly Ile Val Ser
            100                 105                 110

Met Thr Tyr Ser Glu Val Gln Gln Ala Cys Arg Ala Arg Gly Met Arg
        115                 120                 125

Ala Tyr Gly Met Pro Glu His Arg Leu Arg Arg Gln Leu Glu Asp Trp
    130                 135                 140

Ile Asn Leu Ser Leu Asn Glu Lys Val Pro Pro Ser Leu Leu Leu Leu
145                 150                 155                 160

Ser Arg Ala Leu Met Leu Pro Glu Asn Val Pro Val Ser Asp Lys Leu
                165                 170                 175

Lys Ala Thr Ile Asn Ala Leu Pro Glu Thr Ile Val Thr Gln Thr Lys
            180                 185                 190

Ala Ala Ile Gly Glu Arg Glu Gly Lys Ile Asp Asn Lys Thr Lys Ile
        195                 200                 205

Glu Val Ile Lys Glu Glu Glu Arg Lys Ile Arg Glu Glu Arg Gln Glu
    210                 215                 220

Ala Arg Glu Glu Glu Glu Gln Arg Lys Gln Ala Glu Leu Ala Leu Asn
225                 230                 235                 240

Ala Ser Ser Ala Ala Ala Glu Ala Ser Ser Ala Gln Glu Leu Leu Ile
                245                 250                 255

Asp Thr Ala Pro Val Ile Asp Ala Glu Lys Thr Pro Lys Val Ala Thr
            260                 265                 270

Ser Pro Val Glu Ser Pro Leu Ala Pro Pro Glu Val Leu Ile Met Gly
        275                 280                 285

Ala Pro Lys Thr Pro Val Ala Thr Glu Val Asp Lys Asn Ala Asp Glu
    290                 295                 300

Val Glu Phe Thr Lys Lys Asp Leu Glu Val Val Glu Asp Ala Leu Asp
305                 310                 315                 320

Thr Leu Ser Lys Asp Lys Asn Asn Leu Val Ile Glu Lys Glu Val Ile
                325                 330                 335

Lys Asp Ile Lys Glu Glu Ile Ala Asp Tyr Gln Glu Asp Val Glu Glu
            340                 345                 350

Leu Lys Glu Ala Ile Val Ala Ala Glu Lys Pro Lys Asp Glu Ile Lys
        355                 360                 365

Glu Thr Lys Gly Ala Gln Arg Leu Leu Lys Xaa Val Asn Lys Met Ile
```

```
    370                 375                 380

Thr Lys Met Asp Thr Val Val Gln Glu Ile Glu Ser Lys Glu Ser Glu
385                 390                 395                 400

Lys Lys Ala Lys Thr Leu Pro Leu Glu Ala Pro Arg Ser Ala Thr Glu
                405                 410                 415

Thr Gln Glu Leu Asp Val Arg Lys Glu Arg Gly Glu Ile Leu Ile Asp
            420                 425                 430

Glu Leu Met Asp Ala Ile Lys Lys Val Lys Asn Val Pro Asp Glu Asn
        435                 440                 445

Arg Leu Lys Leu Ile Glu Asn Ile Leu Gly Arg Ile Asp Thr Asp Lys
    450                 455                 460


Asp Arg His Ile Lys Val Glu Asp Val Leu Lys Val Ile Asp Ile Val
465                 470                 475                 480

Glu Lys Glu Asp Gly Ile Met Ser Thr Lys Gln Leu Asp Glu Leu Val
                485                 490                 495

Gln Leu Leu Lys Lys Glu Glu Val Ile Glu Leu Glu Glu Lys Lys Glu
            500                 505                 510

Lys Gln Glu Ser Gln Gln Lys Ser Phe Val Pro Pro Ser Glu Thr Leu
        515                 520                 525

His Leu Glu Ser Ser Gln Gln Lys Ser Thr Val Pro Ser Ser Gly His
    530                 535                 540

Glu Ala Lys Val Ser Glu Asp Asp Leu Asn Val Lys Asn Lys Asn Leu
545                 550                 555                 560

Glu Glu Ser Thr Lys Thr Glu Cys Gly Ala Ile Asp Glu Glu His Arg
                565                 570                 575

Arg Glu His Cys Gln Tyr Pro Asp Ile Thr
            580                 585
```

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 293 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```
CCCGGGCTGC AGGAATTCGG CACGAGATGA GAATGGAAAT GTGATTAGCT ATACTGATGA      60

AAATGGAAAC ATTATCAGTA CTACTGATGA GAATGGAAAT GTGATTAGCA TTACTGATGA     120
```

AAATGGAAAT GTGATTAGCA TTACTGATGA AAATGGAAAC ATTATCAGTA CTACTGATGA 180

GAATGGAAAT GTGATTAGCA TTACTGATGA AAATGGAAAT GTGATTAGCA TTACTGATGA 240

AAATGGAAAC ATTATTAGTA CTACTGATGA GAATGGAAAT GTGATTAGCA ATA 293

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 335 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TTGGAAACAG CTATGACCAT GATTACCCCA AGCTCGAAAG TTAAVCCCTC ACTHARAGGG 60

GAACAAAAGT CTGGAGCTCC ACCCGCGGAT GGCGGCCGCB TCTAGAACCT AGTGGACTCC 120

CCCGGSGCTG CAGGAATTCG GGCACGAGCT CCAGCTAGCC ATATACATTC ATCCAAAATG 180

AAGTTGSAAT GTGTCCTACC CGGCAACGGG ATGCCAGAAA TTGTKTCGAA ATKTGTGGAC 240

GAGCACAAGC TTCGTGTCTK TCTATGAAAA ACGTATGGGA GCAGAAGTCG AGGGCCGACA 300

TCCTCGGCGA TGAATGGARA GGTTATGTGC TCCGA 335

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 396 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATAGCTTTTA ATATTTTTAA TTGATGTATT GCTCAATGGT GATTTCTGTT TATTAAACTG 60

AGTTACCAAT ATGCTCGCTT CAATAGACAT AGCAAATGAA AGCATTCCGT ATCCTCAAGC 120

GTTACCAAAC TAACATTAAG GAGTTAAATA AATGTTGTTT CCAATAAATA TAATGGGAAA 180

AACATTTAAT ATTTGTTCCA ATTTGTATTT ATTTTTACTA CAATTATATA CAATAAAATA 240

TTTTTATATA TATTTTATAA AGTTTATGAT GCAGGAGAGA AAATAATGTT AAGAATATAG 300

GTAATGTGTA TATATAAATG TTTGACAAGC ATGTTCTAGT TAAATAATAA ATACAATGTT 360

AAATCTACTT AAAAAAAAAA AAAAAAAAAA AAAAAA 396

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 285 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGAAAGCGAA GAATGAAAAG GGGAAACAAA AAAAGAAAAG ACGAAGGAGT GGAGAGATAA 60

AACGGAGGCA AAGAAGAAAA TGAGGATGCA AAAGAAAGGT AATAAAAGAG ATGAAAAGAA 120

GGAAAAAGGA AATAAGAAAG AAAGAGTGAG GGAAAAATAA AGACAGAGGC GAAGCAAAAA 180

AGGAGGAGAA ATAGAGATTA AAAAAGAAAT ACAGCGAAGA AACCAGGAAA GCGATAAAGA 240

AAAAAAAAGA AAAAAAGAGA GCAGTGAAAA AAAAAAAAAA AAAAA 285

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 228 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CAGATATTTA CTAAAYATTG TGAAAYAAAT CATTTTCAAA ATGGTSTCCA AAGTGTTTGT 60

TGCTCTTGCC ATCAATGGCT TTATAGGGGG CTSCACAAGY CTTTTTTCGA ACAAGATGMC 120

GTCTTAGATA ASATSGTAGA TRACATCTCT GRCTSMATAT GAGAACARCA TTGSMAGAAT 180

TAGCCAAGGR TNGCRAAATT GATATGMTTS CYGCTGTAAT TCGAAAAA 228

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```
CTT CGT GTC AAC CGC TGG GTC AGA CCT GTT ATT GCT ATG CAC CCA ACC        48
Leu Arg Val Asn Arg Trp Val Arg Pro Val Ile Ala Met His Pro Thr
  1               5                  10                  15

ATG ACT CTT GCT GAA CGT CTC GGC AAA AAA GCT TTG CGC GAC CAA TAT        96
Met Thr Leu Ala Glu Arg Leu Gly Lys Lys Ala Leu Arg Asp Gln Tyr
             20                  25                  30

GCT CCC GTT TGC TCC ATT GGA CAA CGT AAC ATC AAC ACC TTT GAC AAC       144
Ala Pro Val Cys Ser Ile Gly Gln Arg Asn Ile Asn Thr Phe Asp Asn
         35                  40                  45

ATG ACC TTC CCC GCT CAA TTC GGA AAA TGC TGG CAC GCT TTG TTG CAA       192
Met Thr Phe Pro Ala Gln Phe Gly Lys Cys Trp His Ala Leu Leu Gln
     50                  55                  60

ACT GTT CCC CAA AAG TAT TCC GAA GAA CGT GAA TAC AGC GAA GAA CAA       240
Thr Val Pro Gln Lys Tyr Ser Glu Glu Arg Glu Tyr Ser Glu Glu Gln
 65                  70                  75                  80

CAA TAC GAC CGT CAA ATG TCC GTC CTC GTT CGT GAA AAC GGC GAA GAA       288
Gln Tyr Asp Arg Gln Met Ser Val Leu Val Arg Glu Asn Gly Glu Glu
                 85                  90                  95

AAA AGA CGT TAT GAT TGT CTT GGG CAA CCG TTA CAA CAA TTG AAT TGC       336
Lys Arg Arg Tyr Asp Cys Leu Gly Gln Pro Leu Gln Gln Leu Asn Cys
            100                 105                 110

AAT                                                                  339
Asn
```

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```
Leu Arg Val Asn Arg Trp Val Arg Pro Val Ile Ala Met His Pro Thr
  1               5                  10                  15

Met Thr Leu Ala Glu Arg Leu Gly Lys Lys Ala Leu Arg Asp Gln Tyr
             20                  25                  30
```

```
Ala Pro Val Cys Ser Ile Gly Gln Arg Asn Ile Asn Thr Phe Asp Asn
         35                  40                  45

Met Thr Phe Pro Ala Gln Phe Gly Lys Cys Trp His Ala Leu Leu Gln
     50                  55                  60

Thr Val Pro Gln Lys Tyr Ser Glu Glu Arg Glu Tyr Ser Glu Glu Gln
 65                  70                  75                  80

Gln Tyr Asp Arg Gln Met Ser Val Leu Val Arg Glu Asn Gly Glu Glu
                 85                  90                  95

Lys Arg Arg Tyr Asp Cys Leu Gly Gln Pro Leu Gln Gln Leu Asn Cys
            100                 105                 110

Asn
```

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 493 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```
TCC AGC TCC TCC AGC TCC AGC AGT GAC TCT TCC AGC TCC AGC AGC TCT      48
Ser Ser Ser Ser Ser Ser Ser Ser Asp Ser Ser Ser Ser Ser Ser Ser
  1               5                  10                  15

TCC TCT TCC AGC TCC AGC AGC TCC TCT TCT GAA TCT TCC GAA GAA AAA      96
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Glu Ser Ser Glu Glu Lys
            20                  25                  30

ACC TCC CAC AAA AAA TCC GAA AAG AAG GAA CAC AAA TCC TGC TCC ATC     144
Thr Ser His Lys Lys Ser Glu Lys Lys Glu His Lys Ser Cys Ser Ile
         35                  40                  45

AAG AAG CAA GTA CAA TTC GTA GAA AAA GAC GGT AAA CTC TGC TTC AGC     192
Lys Lys Gln Val Gln Phe Val Glu Lys Asp Gly Lys Leu Cys Phe Ser
     50                  55                  60

ATC CGT CCC TTG GCC GCT TGC CAA AAA CAC TGC AAA GCC ACT GAA ACC     240
Ile Arg Pro Leu Ala Ala Cys Gln Lys His Cys Lys Ala Thr Glu Thr
 65                  70                  75                  80

ACT CAA ATG GAA GTC GAA GTA TAC TGC CCC TCT GGC AGC CTT GCT GAA     288
Thr Gln Met Glu Val Glu Val Tyr Cys Pro Ser Gly Ser Leu Ala Glu
                 85                  90                  95

CTT TAC AAA CAA AAG ATC CTT AAG GGA GCC AAC CCC GAC TTG AGC GAC     336
```

```
Leu Tyr Lys Gln Lys Ile Leu Lys Gly Ala Asn Pro Asp Leu Ser Asp
           100                 105                 110

AAG ACT CCT TCC AGA ATC TTG AAA TTC AAG GTT CCC AAA GCT TGC ACC       384
Lys Thr Pro Ser Arg Ile Leu Lys Phe Lys Val Pro Lys Ala Cys Thr
        115                 120                 125

GCT TAC TAAATCTGAA ATAAATTACA TGGATTAGTT CATTTCTGAT GTAGTGCAAT       440
Ala Tyr
    130

TAGTTCGATA ATAAATTATT CAATGAGCAT TTAAAAAAAA AAAAAAAAAA AAC           493
```

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```
Ser Ser Ser Ser Ser Ser Ser Ser Asp Ser Ser Ser Ser Ser Ser Ser
  1               5                  10                  15

Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Glu Ser Ser Glu Glu Lys
             20                  25                  30

Thr Ser His Lys Lys Ser Glu Lys Lys Glu His Lys Ser Cys Ser Ile
         35                  40                  45

Lys Lys Gln Val Gln Phe Val Glu Lys Asp Gly Lys Leu Cys Phe Ser
     50                  55                  60

Ile Arg Pro Leu Ala Ala Cys Gln Lys His Cys Lys Ala Thr Glu Thr
 65                  70                  75                  80

Thr Gln Met Glu Val Glu Val Tyr Cys Pro Ser Gly Ser Leu Ala Glu
                 85                  90                  95

Leu Tyr Lys Gln Lys Ile Leu Lys Gly Ala Asn Pro Asp Leu Ser Asp
            100                 105                 110

Lys Thr Pro Ser Arg Ile Leu Lys Phe Lys Val Pro Lys Ala Cys Thr
        115                 120                 125

Ala Tyr
    130
```

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GTAGTGCCAT CATTCGTAAA CSTTYTGACG GTKGGGCGCT GTATWGGTGC TGCCTGGAAA 60

TTGCATCGAT GCACTWCCGT GTCGGGCGCA WATAGTGCKK TGGSCCCTGT CTGMTTATAG 120

ACATTCAGGG CGCSGGSAKT AGCCATGTTC ATGGCTCMCA AWMTGCATTC ACAGTGGGGT 180

CACATTTCAG TCGCATGATT KMTCAARTTA GTATMWGADA TATATTTTTA TCATACTAAG 240

TAGTGAGCDA ATAACACGCG ARWWACRAAC ACCGAATATC TTKAGTTTTT GCACAGATAT 300

KTGTAA 306

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 490 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ACCGGATACG TTGCCAATGA CTACGTCACC ACCAATGTTG TTTCCACTCC AGTTACTGGA 60

TACACCACCG GACATCTTGC TAATGACTAC GTCACCACCA ATGTTGTATC CACTCCAGTT 120

ACTGGATACA CCACCGGACA TCTTGCCAAT GACTACGTCA CCACCAACGT AGTTTCCGCA 180

CCAGTCACCA CTGGATACAC CACTGGCTAT ACCACCGGTA ATGTCGGATA CACCACCGGA 240

GTTACTGGTT ACACCAACGG AGTTAGTGGA TATACCAATG GACTTAATGG TTATACCACT 300

GGTAGCTATG TCAGCTCCCC AGGATACACT TCTTCTGGAC TTGTCAACGT TTTCTAGATT 360

TATGATTTCG TCTGCCCTCA ATGATGATGA CCACACTTTT TACTTTTTAT GATATTTGGA 420

AAAAATAAAT AACTGGAAGA ATATATAATA ATTTCAAAAT AAAAAAAAAA AAAAAAAAAA 480

CTCGAGGGGG 490

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 616 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AAAAAATCGA AAGAAGGCGT AAAACCAAAA TGGGCACAGA AGGATATTCG GGATTTTAGT 60

GATGCCGACA TGGAGAGGTT ACTGGATCAA TGGGAAGAAG ATGAAGACCC CCTTCCAGAA 120

GACGAATTGC CCGAACATCT CAGACCTGAT CCAAAGATCG ACATAAGCAA CATCGATATG 180

AGCAATCCCB AAAACATACT AAAGGCTTCC AAAAAAGGCA AGACTTTGAT GGCATTCGTA 240

CAAGTCAGTG GAAATCCAAC ACAAGAAGAA GCCGAAACCA TCACTAAATT GTGGCAAGGC 300

AGTCTATGGA ATAGTCATAT ACAAGCCGAA AGATATATGG TTAGCGATGA CAGGGCTATA 360

TTTATGTTTA AAGATGGTTC TCAAGCTTGG CCTGCTAAAG ACTTTTTAGT GGAACAAGAA 420

AGGTGTAAAG ATGTTACAAT TGAAAATAAA ATATATCCTG GTAAATATTC TTCGACTAAA 480

GAAGAATTAT AATATAATAT ATTATAATTA TAATCTATAA AATAGATTTG AAATTCTACA 540

TTCATGATCT ACTATGTATG ATATTAATTT ATTAAAAATA ATGTTTTTTC AAGTAAAAAA 600

AAAAAAAAAA AAAAAA 616

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 475 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTCGTGCGGG ACAGATATAG GACCGGATTC GTTAATTGAT TTGAGTGAAG TGGCTTCTGG 60

TGGTTCTGAT ATTGACACAA AATTTTCCAA TTTAAAAATA GATAAAAAGC CTGTTGCAAC 120

TTCACAACAA GGAATTGATG AATTTGATAT GTTTGCACAA TCGAGAAACA TTTCTAGTGA 180

GGGATCAACC AGTGCTATGA AGGAAGGACA CGGTTTGGAC TTATTATCAA ATACACATAA 240

AAATGTACCA CCAACAATTC CACAAGCCGG ACAACTTCCA AGGGATTCTG AGTTTGATGA 300

AATTGCTGCT TGGCTTGATG AAAAGGTTGA AGACAAAGCC CAAGTTCCCG AAGACAGTAT 360

TACAAGCAGT GAATTTGATA AATTCCTGGC AGAACGGGCA GCTGTTGCTG AAACTTTGCC 420

AAATATTCCA CCGACTACAC AAAGTAATCA TTCAAATATT GAAGCAAACG ATAAA 475

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 295 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CCGGCACGGG AGGTAGTGAC GAAAAATAAC GATACGGGAC TCATCCGAGG CCCCGTAATC 60

GGAATGAGTA CACTTTAAAT CCTTTAACGA GGATCTATTA GAGGGCCAGT CTGTGTGCCA 120

GCAGCCGCGG TAATTCCAGC TCTAATAGCG TATATTAAAG TTGTTGCGGT TAAAAAGCTC 180

GTAGTTGAAT CTGTGTCCCA CACTGTYGGT TCACCGCTCG CGGTGTTCAA CTGGCATGTC 240

TGTGGGACGT CCTACCGGTG GGCTTAGCCC GTCAAAAGGC GGCCCAACTC AAAAT 295

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 372 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CTGACTAATC CCAGGACTCC TTTATCCTGT TTGCGCAATG TCGATACCCA TCTCACAATG 60

GTTAATGATT TATCGGCTAA ACAGAAGAGT CCTAAGAAGG TTGTTAAAGG TGTTTCTAGA 120

ATACCGACTT TTAGACCCAA GGCTATGAAT GCTGATGTTG AGAATTTTGA TTCGATGAGG 180

TGCGATGTTT GGRACAAAGA CACCAGTGTT GTTATATAAT TACTAAAGCA ATCCACATGT 240

AGCTAATTTT TTTTTTACAA TTTTATTTGT AACTATGTGT ATTTATATGA ATTCTTGTGG 300

AATATAATTT TAAGTTTTTA AATGAAATAT AGATATTATT CTAAAAAAAA AAAACAAAAA 360

AAAAAAAAAA AA 372

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGATTCGGCA CGAGAATTTA TTAAGCGCAT TATTTGCAAG TGTAATTTGC TCCTTTAACG 60

CGGAAGTACA AAATCGAATC GTTGGTGGCA ATGATGTAAG TATTTCAAAA ATTGGGTGGC 120

AAGTATCTAT TCAAAGTAAT AACCAACATT TCTGTGGTGG TTCAATCATT GCTAAAGATT 180

GGGTACTGAC TTCTTCTCAA TGCGTCGTGG ACAAACAAAG TCCACCGAAG GATTTAACTG 240

TTCGTGTTGG AA 252

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 613 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ATTCCTGCTG TTAATAGTAC TAATGCAGTA ATTGCTGCHA GCTGCTGCAC AGAGGTTTTT 60

AAAATGGCAA CAAGTTGTTA CACCCACATG AACAACTACA TGGTATTCAA TGATACCGAT 120

GGGATTTATA CATATACTTA CGAAGCTGAA AGAAAACCTG ACTGTTTAGC TTGTTCACAA 180

ATTCCAAAAA CTATAGAAGT TTCTAATCCT GAAAATATGA CTCTCCAAGA CTTGATTACT 240

TTGTTGTGTG AAGGGGCTGA ATATCAAATG AAGAGCCCAG GTATTGTAGC CTCAATCGAA 300

GGCAAAAACA AAACCTTATA CATGTCAACA GTAGCAAGTA TAGAAGAAAA GACTAAACAG 360

AATCTAACAA AGTCTCTAAA AGAATTAAAT CTAGAAAATG GAATGGAACT GATGGTTGCA 420

GATGTGACGA CACCAAACAC AATATTACTT AAATTAAAAT ATAAGAATGT AATTGAAAAC 480

GATGTTGAGA TGACTTGATA TTTACTTAAA AATGTTATCT TACAATAATT GATAATTTAT 540

ATTTAATACT TTTGGAACTT TGTATTTAAT GATAATAAAT TATTATAAGA ATTAAAAAAA 600

AAAAAAAAAA AAA 613

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 538 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 3..538

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

```
TT GAT ATT TGC TCT GTT GAG GGT GCC TTA GGA TTT TTA GTG GAA ATG          47
   Asp Ile Cys Ser Val Glu Gly Ala Leu Gly Phe Leu Val Glu Met
     1               5                  10                  15

TTA AAA TAT AAG GCC CCA AGT AAA ACT CTA GCT ATT GTA GAG AAT GCT         95
Leu Lys Tyr Lys Ala Pro Ser Lys Thr Leu Ala Ile Val Glu Asn Ala
                 20                  25                  30

GGT GGA ATA TTA CGA AAT GTA TCT AGT CAT ATA GCC CTT AGA GAG GAC        143
Gly Gly Ile Leu Arg Asn Val Ser Ser His Ile Ala Leu Arg Glu Asp
             35                  40                  45

TAC AGA GAA ATA CTT CGA CAT CAT AAT TGC TTA ACA ATA TTA CTA CAA        191
Tyr Arg Glu Ile Leu Arg His His Asn Cys Leu Thr Ile Leu Leu Gln
         50                  55                  60

CAA TTA AAA TCA CCA AGC CTC ATA ATT GTC AGT AAT GCT TGT GGG ACA        239
Gln Leu Lys Ser Pro Ser Leu Ile Ile Val Ser Asn Ala Cys Gly Thr
     65                  70                  75

TTA TGG AAT TTA TCT GCT AGG AAT TCA ACA GAT CAA CAA TTT TTA TGG        287
Leu Trp Asn Leu Ser Ala Arg Asn Ser Thr Asp Gln Gln Phe Leu Trp
 80                  85                  90                  95

GAG AAT GGT GCT GTC CCT TTA TTA AGA AGT TTG ATA TAT TCT AAG CAT        335
Glu Asn Gly Ala Val Pro Leu Leu Arg Ser Leu Ile Tyr Ser Lys His
                100                 105                 110

AAA ATG ATA TCT ATG GGA TCA AGT GCA GCT CTC AAA AAT TTG TTA AAT        383
Lys Met Ile Ser Met Gly Ser Ser Ala Ala Leu Lys Asn Leu Leu Asn
            115                 120                 125

GCA AAA CCT GAG TGC ATC AAT TTC TTA AGT GAT TCT TCT TCT AAA GGA        431
Ala Lys Pro Glu Cys Ile Asn Phe Leu Ser Asp Ser Ser Ser Lys Gly
        130                 135                 140

GTT CCA AAT CTA ACT ACA TTG GGT GTA AGA AAA CAA AAA TCT CTA CAT        479
Val Pro Asn Leu Thr Thr Leu Gly Val Arg Lys Gln Lys Ser Leu His
    145                 150                 155

GAG TTA ATA GAT CAA AAT CTT TCA GAA ACT TGT GAT AAT ATA GAT AGT        527
Glu Leu Ile Asp Gln Asn Leu Ser Glu Thr Cys Asp Asn Ile Asp Ser
160                 165                 170                 175

GTG GCC GCT  AA                                                       538
Val Ala Ala
```

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 178 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

```
Asp Ile Cys Ser Val Glu Gly Ala Leu Gly Phe Leu Val Glu Met Leu
 1               5                  10                  15

Lys Tyr Lys Ala Pro Ser Lys Thr Leu Ala Ile Val Glu Asn Ala Gly
            20                  25                  30

Gly Ile Leu Arg Asn Val Ser Ser His Ile Ala Leu Arg Glu Asp Tyr
        35                  40                  45

Arg Glu Ile Leu Arg His His Asn Cys Leu Thr Ile Leu Leu Gln Gln
    50                  55                  60

Leu Lys Ser Pro Ser Leu Ile Ile Val Ser Asn Ala Cys Gly Thr Leu
65                  70                  75                  80

Trp Asn Leu Ser Ala Arg Asn Ser Thr Asp Gln Gln Phe Leu Trp Glu
                85                  90                  95

Asn Gly Ala Val Pro Leu Leu Arg Ser Leu Ile Tyr Ser Lys His Lys
            100                 105                 110

Met Ile Ser Met Gly Ser Ser Ala Ala Leu Lys Asn Leu Leu Asn Ala
        115                 120                 125

Lys Pro Glu Cys Ile Asn Phe Leu Ser Asp Ser Ser Ser Lys Gly Val
    130                 135                 140

Pro Asn Leu Thr Thr Leu Gly Val Arg Lys Gln Lys Ser Leu His Glu
145                 150                 155                 160

Leu Ile Asp Gln Asn Leu Ser Glu Thr Cys Asp Asn Ile Asp Ser Val
                165                 170                 175

Ala Ala
```

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 432 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

```
GTT CTT CTT AAA CAG TTG GAC TCT GGA TTG TTA CTT GTT ACA GGT CCC        48
Val Leu Leu Lys Gln Leu Asp Ser Gly Leu Leu Leu Val Thr Gly Pro
 1               5                  10                  15

TTC TTA ATC AAT GCA TGC CCA TTG CGT CGC ATT TCC CAA AAC TAT GTC        96
```

```
Phe Leu Ile Asn Ala Cys Pro Leu Arg Arg Ile Ser Gln Asn Tyr Val
            20                  25                  30

ATT GCC ACC TCT ACC CGA TTA GAC GTT AGT GGA GTT AAA TTA CCA GAA       144
Ile Ala Thr Ser Thr Arg Leu Asp Val Ser Gly Val Lys Leu Pro Glu
         35                  40                  45

CAC ATC AAT GAT GAT TAT TTC AAA AGG CAA AAG AAC AAG CGT GCA AAG       192
His Ile Asn Asp Asp Tyr Phe Lys Arg Gln Lys Asn Lys Arg Ala Lys
   50                  55                  60

AAA GAG GAA GGT GAT ATT TTT GCT GCC AAG AAA GAG GCT TAT AAA CCA       240
Lys Glu Glu Gly Asp Ile Phe Ala Ala Lys Lys Glu Ala Tyr Lys Pro
 65                  70                  75                  80

ACT GAG CAA AGG AAG AAT GAC CAA AAG CTT GTA GAC AAA ATG GTT TTA       288
Thr Glu Gln Arg Lys Asn Asp Gln Lys Leu Val Asp Lys Met Val Leu
                 85                  90                  95

GGA GTA ATC AAG AAG CAC CCA GAC CAC AAA CTT TTG TAT ACA TAT TTG       336
Gly Val Ile Lys Lys His Pro Asp His Lys Leu Leu Tyr Thr Tyr Leu
            100                 105                 110

TCA GCT ATG TTT GGT TTG AAA TCT TCC CAA TAT CCA CAT CGT ATG AAG       384
Ser Ala Met Phe Gly Leu Lys Ser Ser Gln Tyr Pro His Arg Met Lys
        115                 120                 125

TTC  T AAATACTATA TTCATAAAAT AAATTGAACT TCTCAAAAAA AAAA               432
Phe
```

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 129 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

```
Val Leu Leu Lys Gln Leu Asp Ser Gly Leu Leu Leu Val Thr Gly Pro
 1               5                  10                  15

Phe Leu Ile Asn Ala Cys Pro Leu Arg Arg Ile Ser Gln Asn Tyr Val
            20                  25                  30

Ile Ala Thr Ser Thr Arg Leu Asp Val Ser Gly Val Lys Leu Pro Glu
         35                  40                  45

His Ile Asn Asp Asp Tyr Phe Lys Arg Gln Lys Asn Lys Arg Ala Lys
     50                  55                  60

Lys Glu Glu Gly Asp Ile Phe Ala Ala Lys Lys Glu Ala Tyr Lys Pro
 65                  70                  75                  80

Thr Glu Gln Arg Lys Asn Asp Gln Lys Leu Val Asp Lys Met Val Leu
```

```
                  85                  90                  95

Gly Val Ile Lys Lys His Pro Asp His Lys Leu Leu Tyr Thr Tyr Leu
            100                 105                 110

Ser Ala Met Phe Gly Leu Lys Ser Ser Gln Tyr Pro His Arg Met Lys
        115                 120                 125

Phe
```

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 595 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 47..315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```
TGGAAATTCA ATATTTTGTT TTAACATTAA ATTTTTCAAA TTCGAT ATG AAA TTT        55
                                                    Met Lys Phe
                                                      1

TTA CTG GCA ATT TGC GTG TTG TGT GTT TTA TTA AAT CAA GTA TCT ATG       103
Leu Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln Val Ser Met
      5                  10                  15

TCA AAA ATG GTC ACT GAA AAG TGT AAA TCG GGA GGA AAT AAT CCA AGT       151
Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn Asn Pro Ser
 20                  25                  30                  35

ACA AAA GAG GTG TCA ATA CCA TCT GGG AAG CTT ACT ATT GAA GAT TTT       199
Thr Lys Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile Glu Asp Phe
                 40                  45                  50

TGT ATT GGA AAT CAT CAA AGT TGC AAA ATA TTT TGC AAA AGT CAA TGT       247
Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Cys Lys Ser Gln Cys
             55                  60                  65

GGA TTT GGA GGT GGT GCT TGT GGA AAC GGT GGT TCA ACA CGA CCA AAT       295
Gly Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr Arg Pro Asn
         70                  75                  80

CAA AAA CAC TGT TAT TGC GA ATAACCATAT TCCGGATGAA AGACCAAATT           345
Gln Lys His Cys Tyr Cys
     85

GATATAAATT ACTAAAATTA TGCTAGATAG CAATCATAAA ATTTTGAAGT TTTCAATGAT     405
```

CCTAACATGT TTTGCCTCCA ATTTATTTTA ACAGCAAATT GCTGGGAACT TACCGTACCG 465

TAACAAAATG TTCAAGAAAT ACTGAATGTT TACAAATAGA TTATTATAAA TATTGTAACA 525

TTGTCTAATA TTTATAAGAA TTATATAAAC TGAATTGCAA AAGTTGAAAA AAAAAAAAAA 585

AAAAAAAAAA 595

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Met Lys Phe Leu Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln
1 5 10 15

Val Ser Met Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn
20 25 30

Asn Pro Ser Thr Lys Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile
35 40 45

Glu Asp Phe Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Cys Lys
50 55 60

Ser Gln Cys Gly Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr
65 70 75 80

Arg Pro Asn Gln Lys His Cys Tyr Cys
85

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 595 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TTTTTTTTTT TTTTTTTTTT TTTTCAACTT TTGCAATTCA GTTTATATAA TTCTTATAAA 60

TATTAGACAA TGTTACAATA TTTATAATAA TCTATTTGTA AACATTCAGT ATTTCTTGAA 120

CATTTTGTTA CGGTACGGTA AGTTCCCAGC AATTTGCTGT TAAAATAAAT TGGAGGCAAA 180

```
ACATGTTAGG ATCATTGAAA ACTTCAAAAT TTTATGATTG CTATCTAGCA TAATTTTAGT     240

AATTTATATC AATTTGGTCT TTCATCCGGA ATATGGTTAT TCGCAATAAC AGTGTTTTTG     300

ATTTGGTCGT GTTGAACCAC CGTTTCCACA AGCACCACCT CCAAATCCAC ATTGACTTTT     360

GCAAAATATT TTGCAACTTT GATGATTTCC AATACAAAAA TCTTCAATAG TAAGCTTCCC     420

AGATGGTATT GACACCTCTT TTGTACTTGG ATTATTTCCT CCCGATTTAC ACTTTTCAGT     480

GACCATTTTT GACATAGATA CTTGATTTAA TAAAACACAC AACACGCAAA TTGCCAGTAA     540

AAATTTCATA TCGAATTTGA AAAATTTAAT GTTAAAACAA AATATTGAAT TTCCA          595
```

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 270 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

```
ATG AAA TTT TTA CTG GCA ATT TGC GTG TTG TGT GTT TTA TTA AAT CAA        48
Met Lys Phe Leu Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln
  1               5                  10                  15

GTA TCT ATG TCA AAA ATG GTC ACT GAA AAG TGT AAA TCG GGA GGA AAT        96
Val Ser Met Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn
             20                  25                  30

AAT CCA AGT ACA AAA GAG GTG TCA ATA CCA TCT GGG AAG CTT ACT ATT       144
Asn Pro Ser Thr Lys Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile
         35                  40                  45

GAA GAT TTT TGT ATT GGA AAT CAT CAA AGT TGC AAA ATA TTT TGC AAA       192
Glu Asp Phe Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Cys Lys
     50                  55                  60

AGT CAA TGT GGA TTT GGA GGT GGT GCT TGT GGA AAC GGT GGT TCA ACA       240
Ser Gln Cys Gly Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr
 65                  70                  75                  80

CGA CCA AAT CAA AAA CAC TGT TAT TGC GAA                              270
Arg Pro Asn Gln Lys His Cys Tyr Cys Glu
                 85                  90
```

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

```
Met Lys Phe Leu Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln
 1               5                  10                  15

Val Ser Met Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn
            20                  25                  30

Asn Pro Ser Thr Lys Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile
        35                  40                  45

Glu Asp Phe Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Cys Lys
    50                  55                  60

Ser Gln Cys Gly Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr
65                  70                  75                  80

Arg Pro Asn Gln Lys His Cys Tyr Cys Glu
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 270 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

```
TTCGCAATAA CAGTGTTTTT GATTTGGTCG TGTTGAACCA CCGTTTCCAC AAGCACCACC      60

TCCAAATCCA CATTGACTTT TGCAAAATAT TTTGCAACTT TGATGATTTC CAATACAAAA     120

ATCTTCAATA GTAAGCTTCC CAGATGGTAT TGACACCTCT TTTGTACTTG GATTATTTCC     180

TCCCGATTTA CACTTTTCAG TGACCATTTT TGACATAGAT ACTTGATTTA ATAAAACACA     240

CAACACGCAA ATTGCCAGTA AAAATTTCAT                                      270
```

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

```
TCA AAA ATG GTC ACT GAA AAG TGT AAA TCG GGA GGA AAT AAT CCA AGT        48
Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn Asn Pro Ser
  1               5                  10                  15

ACA AAA GAG GTG TCA ATA CCA TCT GGG AAG CTT ACT ATT GAA GAT TTT        96
Thr Lys Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile Glu Asp Phe
            20                  25                  30

TGT ATT GGA AAT CAT CAA AGT TGC AAA ATA TTT TGC AAA AGT CAA TGT       144
Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Cys Lys Ser Gln Cys
        35                  40                  45

GGA TTT GGA GGT GGT GCT TGT GGA AAC GGT GGT TCA ACA CGA CCA AAT       192
Gly Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr Arg Pro Asn
    50                  55                  60

CAA AAA CAC TGT TAT TGC GAA                                          213
Gln Lys His Cys Tyr Cys Glu
65                  70
```

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

```
Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn Asn Pro Ser
  1               5                  10                  15

Thr Lys Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile Glu Asp Phe
            20                  25                  30

Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Cys Lys Ser Gln Cys
        35                  40                  45

Gly Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr Arg Pro Asn
    50                  55                  60

Gln Lys His Cys Tyr Cys Glu
65                  70
```

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

```
TTCGCAATAA CAGTGTTTTT GATTTGGTCG TGTTGAACCA CCGTTTCCAC AAGCACCACC      60

TCCAAATCCA CATTGACTTT TGCAAAATAT TTTGCAACTT TGATGATTTC CAATACAAAA     120

ATCTTCAATA GTAAGCTTCC CAGATGGTAT TGACACCTCT TTTGTACTTG GATTATTTCC     180

TCCCGATTTA CACTTTTCAG TGACCATTTT TGA                                  213
```

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1007 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

```
TGG AAA GTT AAT AAA AAA TGT ACA TCA GGT GGA AAA AAT CAA GAT AGA       48
Trp Lys Val Asn Lys Lys Cys Thr Ser Gly Gly Lys Asn Gln Asp Arg
  1               5                  10                  15

AAA CTC GAT CAA ATA ATT CAA AAA GGC CAA CAA GTT AAA ATC CAA AAT       96
Lys Leu Asp Gln Ile Ile Gln Lys Gly Gln Gln Val Lys Ile Gln Asn
            20                  25                  30

ATT TGC AAA TTA ATA CGA GAT AAA CCA CAT ACA AAT CAA GAG AAA GAA      144
Ile Cys Lys Leu Ile Arg Asp Lys Pro His Thr Asn Gln Glu Lys Glu
        35                  40                  45


AAA TGT ATG AAA TTT TGC AAA AAA GTT TGC AAA GGT TAT AGA GGA GCT      192
Lys Cys Met Lys Phe Cys Lys Lys Val Cys Lys Gly Tyr Arg Gly Ala
    50                  55                  60

TGT GAT GGC AAT ATT TGC TAC TGC AGC AGG CCA AGT AAT TTA GGT CCT      240
Cys Asp Gly Asn Ile Cys Tyr Cys Ser Arg Pro Ser Asn Leu Gly Pro
65                  70                  75                  80

GAT TGG AAA GTA AGC AAA GAA TGC AAA GAT CCC AAT AAC AAA GAT TCT      288
Asp Trp Lys Val Ser Lys Glu Cys Lys Asp Pro Asn Asn Lys Asp Ser
                85                  90                  95
```

```
CGT CCT ACG GAA ATA GTT CCA TAT CGA CAA CAA TTA GCA AAT CCA AAT       336
Arg Pro Thr Glu Ile Val Pro Tyr Arg Gln Gln Leu Ala Asn Pro Asn
            100                 105                 110

ATT TGC AAA CTA AAA AAT TCA GAG ACC AAT GAA GAT TCC AAA TGC AAA       384
Ile Cys Lys Leu Lys Asn Ser Glu Thr Asn Glu Asp Ser Lys Cys Lys
        115                 120                 125

AAA CAT TGC AAA GAA AAA TGT CGT GGT GGA AAT GAT GCT GGA TGT GAT       432
Lys His Cys Lys Glu Lys Cys Arg Gly Gly Asn Asp Ala Gly Cys Asp
    130                 135                 140

GGA AAC TTT TGT TAT TGT CGA CCA AAA AAT AAA TAATAATTAT AATAAATAAA     485
Gly Asn Phe Cys Tyr Cys Arg Pro Lys Asn Lys
145                 150                 155

TTGTTATAGT TATTAGTTAT CCCATCACAT ATTAGAAAAG TGGCTTATAA TTTATGAACA     545

ATATAACACA TAAATTAGTT GTGTAATTTC GAATGTTTTT TTCAAATATA AGGCGTTTTT     605

CTAGAATATC TTGATATTAG AAACTAACTT AGATTATTTT GTTGTGTATA AAATATTCAA     665

ATACGTAAGT TATATTGAAC AAAGCATTTA GAAGCTACAT TAGATATACT AAATAAGTGC     725

AAAATTGCAT GGAAACCCTT ACTGGATTTA CTACATATTT TCTTCCTAAA TATTGTCTTG     785

GTATTACTCT TATTATATAA AAATTAATAT AAAATTGTAG ACAGAGACGA ATTGGGGTAT     845

TGTTATATAT AAAAAAGTAG TGGATTATTT AATTCTAAAA AAGTTTGCAA AATGTTTCAT     905

ACATAATAAC CGAATATTTT CAAATATATA AATATTGTAA TGAATAAATG CGCATCTGTA     965

TGCTTAATAT AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA                       1007
```

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

```
Trp Lys Val Asn Lys Lys Cys Thr Ser Gly Gly Lys Asn Gln Asp Arg
  1               5                  10                  15

Lys Leu Asp Gln Ile Ile Gln Lys Gly Gln Gln Val Lys Ile Gln Asn
            20                  25                  30

Ile Cys Lys Leu Ile Arg Asp Lys Pro His Thr Asn Gln Glu Lys Glu
        35                  40                  45

Lys Cys Met Lys Phe Cys Lys Lys Val Cys Lys Gly Tyr Arg Gly Ala
    50                  55                  60
```

```
Cys Asp Gly Asn Ile Cys Tyr Cys Ser Arg Pro Ser Asn Leu Gly Pro
 65                  70                  75                  80

Asp Trp Lys Val Ser Lys Glu Cys Lys Asp Pro Asn Asn Lys Asp Ser
                 85                  90                  95

Arg Pro Thr Glu Ile Val Pro Tyr Arg Gln Gln Leu Ala Asn Pro Asn
            100                 105                 110

Ile Cys Lys Leu Lys Asn Ser Glu Thr Asn Glu Asp Ser Lys Cys Lys
        115                 120                 125

Lys His Cys Lys Glu Lys Cys Arg Gly Gly Asn Asp Ala Gly Cys Asp
    130                 135                 140

Gly Asn Phe Cys Tyr Cys Arg Pro Lys Asn Lys
145                 150                 155
```

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1007 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

```
TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTATATTAAG CATACAGATG CGCATTTATT      60

CATTACAATA TTTATATATT TGAAAATATT CGGTTATTAT GTATGAAACA TTTTGCAAAC     120

TTTTTTAGAA TTAAATAATC CACTACTTTT TTATATATAA CAATACCCCA ATTCGTCTCT     180

GTCTACAATT TTATATTAAT TTTTATATAA TAAGAGTAAT ACCAAGACAA TATTTAGGAA     240

GAAAATATGT AGTAAATCCA GTAAGGGTTT CCATGCAATT TTGCACTTAT TTAGTATATC     300

TAATGTAGCT TCTAAATGCT TTGTTCAATA TAACTTACGT ATTTGAATAT TTTATACACA     360

ACAAAATAAT CTAAGTTAGT TTCTAATATC AAGATATTCT AGAAAAACGC CTTATATTTG     420

AAAAAAACAT TCGAAATTAC ACAACTAATT TATGTGTTAT ATTGTTCATA AATTATAAGC     480

CACTTTTCTA ATATGTGATG GGATAACTAA TAACTATAAC AATTTATTTA TTATAATTAT     540

TATTTATTTT TTGGTCGACA ATAACAAAAG TTTCCATCAC ATCCAGCATC ATTTCCACCA     600

CGACATTTTT CTTTGCAATG TTTTTTGCAT TTGGAATCTT CATTGGTCTC TGAATTTTTT     660

AGTTTGCAAA TATTTGGAAT TGCTAATTGT TGTCGATATG GAACTATTTC CGTAGGACGA     720

GAATCTTTGT TATTGGGATC TTTGCATTCT TTGCTTACTT TCCAATCAGG ACCTAAATTA     780
```

```
CTTGGCCTGC TGCAGTAGCA AATATTGCCA TCACAAGCTC CTCTATAACC TTTGCAAACT      840

TTTTTGCAAA ATTTCATACA TTTTTCTTTC TCTTGATTTG TATGTGGTTT ATCTCGTATT      900

AATTTGCAAA TATTTTGGAT TTTAACTTGT TGGCCTTTTT GAATTATTTG ATCGAGTTTT      960

CTATCTTGAT TTTTTCCACC TGATGTACAT TTTTTATTAA CTTTCCA                    1007
```

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1205 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 4..1062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

```
GCA GAA TTG AAA TTT GTG TTT GCG ACT GCA CGA GGT ATG TCA CAT ACA        48
    Glu Leu Lys Phe Val Phe Ala Thr Ala Arg Gly Met Ser His Thr
      1               5                  10                  15

CCT TGT GAT TAT CCA GGC GGT CCA AAA ATT ACA CAC AAG TCT GAA GAT        96
Pro Cys Asp Tyr Pro Gly Gly Pro Lys Ile Thr His Lys Ser Glu Asp
                 20                  25                  30

TCA AGC CAA TTG ACA CCG GCA GGT CAA GAA GAG GCA TTA AAA ATT GGC       144
Ser Ser Gln Leu Thr Pro Ala Gly Gln Glu Glu Ala Leu Lys Ile Gly
             35                  40                  45

AAA TTA TTA TCC GAA CAT TAC AGA ACT AAT TTA AAA GTT GAC AAA TGG       192
Lys Leu Leu Ser Glu His Tyr Arg Thr Asn Leu Lys Val Asp Lys Trp
         50                  55                  60

GAT TCA AAT AAA AAT TAT TGG ACA TTA GCT AGT GCT ACG AGA AGA TCT       240
Asp Ser Asn Lys Asn Tyr Trp Thr Leu Ala Ser Ala Thr Arg Arg Ser
     65                  70                  75

CAA GAA GGA GCG CTT ATC ATT GGT TCT GGT CTA GAA GAA AAG GAA AAG       288
Gln Glu Gly Ala Leu Ile Ile Gly Ser Gly Leu Glu Glu Lys Glu Lys
 80                  85                  90                  95

GCA GTT TGG ACA AAA GAG AAA GGA GAT AAA ACC ATA TTT TCT TCG TTT       336
Ala Val Trp Thr Lys Glu Lys Gly Asp Lys Thr Ile Phe Ser Ser Phe
                100                 105                 110

GGT GAA TAT GCT AAA TTT TAT AGT CCA AAA ACT TGT CCA AAC TTC ATA       384
Gly Glu Tyr Ala Lys Phe Tyr Ser Pro Lys Thr Cys Pro Asn Phe Ile
            115                 120                 125

GCA CAA CAG AAA ATA GCA GTA AGA GAC TTG TTA ACA AAA AGT GCA AAA       432
Ala Gln Gln Lys Ile Ala Val Arg Asp Leu Leu Thr Lys Ser Ala Lys
```

```
        130                 135                 140

GAT TAT AAA AAT TCA CTT GCA AAA TTA AAA GAA GCG TAT AAA ATA GAT       480
Asp Tyr Lys Asn Ser Leu Ala Lys Leu Lys Glu Ala Tyr Lys Ile Asp
    145                 150                 155

GCG ACG ACA AGC CCT CAG AAT GTT TGG CTG GCA TAT GAA ACT TTG AAT       528
Ala Thr Thr Ser Pro Gln Asn Val Trp Leu Ala Tyr Glu Thr Leu Asn
160                 165                 170                 175

TTA CAA AGC AAG CAA AAT AAC GCT CCA ACA TGG TGG AAT ACT GTA AAC       576
Leu Gln Ser Lys Gln Asn Asn Ala Pro Thr Trp Trp Asn Thr Val Asn
                180                 185                 190

AAA GAT CTA AAA CAA TTC TCT GAG AAA TAT TTA TGG ACC GCC TTG ACT       624
Lys Asp Leu Lys Gln Phe Ser Glu Lys Tyr Leu Trp Thr Ala Leu Thr
            195                 200                 205

TCT AAT GAT AAT CTT AGA AAG ATG TCA GGA GGT CGT ATG ATT AAC GAT       672
Ser Asn Asp Asn Leu Arg Lys Met Ser Gly Gly Arg Met Ile Asn Asp
        210                 215                 220

ATA TTG AAC GAT ATC GAA AAC ATA AAG AAA GGA GAG GGA CAA CCG GGT       720
Ile Leu Asn Asp Ile Glu Asn Ile Lys Lys Gly Glu Gly Gln Pro Gly
    225                 230                 235

GCT CCA GGA GGA AAG GAA AAC AAA TTA TCA GTG CTG ACC GTT CCT CAA       768
Ala Pro Gly Gly Lys Glu Asn Lys Leu Ser Val Leu Thr Val Pro Gln
240                 245                 250                 255

GCT ATC TTA GCA GCA TTT GTT TCA GCA TTT GCT CCC GAA GGT ACA AAA       816
Ala Ile Leu Ala Ala Phe Val Ser Ala Phe Ala Pro Glu Gly Thr Lys
                260                 265                 270

ATT GAA AAT AAG GAC CTT GAT CCG TCT ACT TTA TAT CCT GGC CAA GGA       864
Ile Glu Asn Lys Asp Leu Asp Pro Ser Thr Leu Tyr Pro Gly Gln Gly
            275                 280                 285

GCA CTT CAC GTT ATT GAA CTA CAC CAA GAT AAG AGC GAT TGG AGC ATA       912
Ala Leu His Val Ile Glu Leu His Gln Asp Lys Ser Asp Trp Ser Ile
        290                 295                 300

AAA GTT CTC TAT AGA AAC AAT GAC CAA ATG AAG CTG AAA CCA ATG AAA       960
Lys Val Leu Tyr Arg Asn Asn Asp Gln Met Lys Leu Lys Pro Met Lys
    305                 310                 315

CTT GCA CAA TGC GGT GAC AAG TGT TCT TAT GGT ACT TTC AAA TCA ATG      1008
Leu Ala Gln Cys Gly Asp Lys Cys Ser Tyr Gly Thr Phe Lys Ser Met
320                 325                 330                 335

CTA CAA AAA TAT AAC ATG GAG AAG GAA GCT CAT GAT AAA TTA TGT AAA      1056
Leu Gln Lys Tyr Asn Met Glu Lys Glu Ala His Asp Lys Leu Cys Lys
                340                 345                 350

ACG TCG TAAAAATTAA AAATAAAAAC TTTTCAATAT ATTTTCCGCT AAAATAAATA       1112
Thr Ser

AATATGTTTG TATATTTAAA CTTATCAAAA TAATAGTAGT GTTTTAATAA AGATTTTAAA    1172
```

TAAATAATTG TAAAAAAAAA AAAAAAAAAA AAA 1205

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 353 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

```
Glu Leu Lys Phe Val Phe Ala Thr Ala Arg Gly Met Ser His Thr Pro
 1               5                  10                  15

Cys Asp Tyr Pro Gly Gly Pro Lys Ile Thr His Lys Ser Glu Asp Ser
            20                  25                  30

Ser Gln Leu Thr Pro Ala Gly Gln Glu Glu Ala Leu Lys Ile Gly Lys
        35                  40                  45

Leu Leu Ser Glu His Tyr Arg Thr Asn Leu Lys Val Asp Lys Trp Asp
    50                  55                  60

Ser Asn Lys Asn Tyr Trp Thr Leu Ala Ser Ala Thr Arg Arg Ser Gln
65                  70                  75                  80

Glu Gly Ala Leu Ile Ile Gly Ser Gly Leu Glu Glu Lys Glu Lys Ala
                85                  90                  95

Val Trp Thr Lys Glu Lys Gly Asp Lys Thr Ile Phe Ser Ser Phe Gly
            100                 105                 110

Glu Tyr Ala Lys Phe Tyr Ser Pro Lys Thr Cys Pro Asn Phe Ile Ala
        115                 120                 125

Gln Gln Lys Ile Ala Val Arg Asp Leu Leu Thr Lys Ser Ala Lys Asp
    130                 135                 140

Tyr Lys Asn Ser Leu Ala Lys Leu Lys Glu Ala Tyr Lys Ile Asp Ala
145                 150                 155                 160

Thr Thr Ser Pro Gln Asn Val Trp Leu Ala Tyr Glu Thr Leu Asn Leu
                165                 170                 175

Gln Ser Lys Gln Asn Asn Ala Pro Thr Trp Trp Asn Thr Val Asn Lys
            180                 185                 190

Asp Leu Lys Gln Phe Ser Glu Lys Tyr Leu Trp Thr Ala Leu Thr Ser
        195                 200                 205

Asn Asp Asn Leu Arg Lys Met Ser Gly Gly Arg Met Ile Asn Asp Ile
    210                 215                 220

Leu Asn Asp Ile Glu Asn Ile Lys Lys Gly Glu Gly Gln Pro Gly Ala
```

225 230 235 240

Pro Gly Gly Lys Glu Asn Lys Leu Ser Val Leu Thr Val Pro Gln Ala
245 250 255

Ile Leu Ala Ala Phe Val Ser Ala Phe Ala Pro Glu Gly Thr Lys Ile
260 265 270

Glu Asn Lys Asp Leu Asp Pro Ser Thr Leu Tyr Pro Gly Gln Gly Ala
275 280 285

Leu His Val Ile Glu Leu His Gln Asp Lys Ser Asp Trp Ser Ile Lys
290 295 300

Val Leu Tyr Arg Asn Asn Asp Gln Met Lys Leu Lys Pro Met Lys Leu
305 310 315 320

Ala Gln Cys Gly Asp Lys Cys Ser Tyr Gly Thr Phe Lys Ser Met Leu
325 330 335

Gln Lys Tyr Asn Met Glu Lys Glu Ala His Asp Lys Leu Cys Lys Thr
340 345 350

Ser

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1205 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

TTTTTTTTTT TTTTTTTTTT TTACAATTAT TTATTTAAAA TCTTTATTAA AACACTACTA 60

TTATTTTGAT AAGTTTAAAT ATACAAACAT ATTTATTTAT TTTAGCGGAA AATATATTGA 120

AAAGTTTTTA TTTTTAATTT TTACGACGTT TTACATAATT TATCATGAGC TTCCTTCTCC 180

ATGTTATATT TTTGTAGCAT TGATTTGAAA GTACCATAAG AACACTTGTC ACCGCATTGT 240

GCAAGTTTCA TTGGTTTCAG CTTCATTTGG TCATTGTTTC TATAGAGAAC TTTTATGCTC 300

CAATCGCTCT TATCTTGGTG TAGTTCAATA ACGTGAAGTG CTCCTTGGCC AGGATATAAA 360

GTAGACGGAT CAAGGTCCTT ATTTTCAATT TTTGTACCTT CGGGAGCAAA TGCTGAAACA 420

AATGCTGCTA AGATAGCTTG AGGAACGGTC AGCACTGATA ATTTGTTTTC CTTTCCTCCT 480

GGAGCACCCG GTTGTCCCTC TCCTTTCTTT ATGTTTTCGA TATCGTTCAA TATATCGTTA 540

ATCATACGAC CTCCTGACAT CTTTCTAAGA TTATCATTAG AAGTCAAGGC GGTCCATAAA 600

TATTTCTCAG AGAATTGTTT TAGATCTTTG TTTACAGTAT TCCACCATGT TGGAGCGTTA 660

```
TTTTGCTTGC TTTGTAAATT CAAAGTTTCA TATGCCAGCC AAACATTCTG AGGGCTTGTC     720

GTCGCATCTA TTTTATACGC TTCTTTTAAT TTTGCAAGTG AATTTTTATA ATCTTTTGCA     780

CTTTTTGTTA ACAAGTCTCT TACTGCTATT TTCTGTTGTG CTATGAAGTT TGGACAAGTT     840

TTTGGACTAT AAAATTTAGC ATATTCACCA AACGAAGAAA ATATGGTTTT ATCTCCTTTC     900

TCTTTTGTCC AAACTGCCTT TTCCTTTTCT TCTAGACCAG AACCAATGAT AAGCGCTCCT     960

TCTTGAGATC TTCTCGTAGC ACTAGCTAAT GTCCAATAAT TTTTATTTGA ATCCCATTTG    1020

TCAACTTTTA AATTAGTTCT GTAATGTTCG GATAATAATT TGCCAATTTT TAATGCCTCT    1080

TCTTGACCTG CCGGTGTCAA TTGGCTTGAA TCTTCAGACT TGTGTGTAAT TTTTGGACCG    1140

CCTGGATAAT CACAAGGTGT ATGTGACATA CCTCGTGCAG TCGCAAACAC AAATTTCAAT    1200

TCTGC                                                                1205
```

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1059 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1059

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```
GAA TTG AAA TTT GTG TTT GCG ACT GCA CGA GGT ATG TCA CAT ACA CCT        48
Glu Leu Lys Phe Val Phe Ala Thr Ala Arg Gly Met Ser His Thr Pro
  1               5                  10                  15

TGT GAT TAT CCA GGC GGT CCA AAA ATT ACA CAC AAG TCT GAA GAT TCA        96
Cys Asp Tyr Pro Gly Gly Pro Lys Ile Thr His Lys Ser Glu Asp Ser
             20                  25                  30

AGC CAA TTG ACA CCG GCA GGT CAA GAA GAG GCA TTA AAA ATT GGC AAA       144
Ser Gln Leu Thr Pro Ala Gly Gln Glu Glu Ala Leu Lys Ile Gly Lys
         35                  40                  45

TTA TTA TCC GAA CAT TAC AGA ACT AAT TTA AAA GTT GAC AAA TGG GAT       192
Leu Leu Ser Glu His Tyr Arg Thr Asn Leu Lys Val Asp Lys Trp Asp
     50                  55                  60

TCA AAT AAA AAT TAT TGG ACA TTA GCT AGT GCT ACG AGA AGA TCT CAA       240
Ser Asn Lys Asn Tyr Trp Thr Leu Ala Ser Ala Thr Arg Arg Ser Gln
 65                  70                  75                  80

GAA GGA GCG CTT ATC ATT GGT TCT GGT CTA GAA GAA AAG GAA AAG GCA       288
```

```
Glu Gly Ala Leu Ile Ile Gly Ser Gly Leu Glu Glu Lys Glu Lys Ala
                 85                  90                  95

GTT TGG ACA AAA GAG AAA GGA GAT AAA ACC ATA TTT TCT TCG TTT GGT       336
Val Trp Thr Lys Glu Lys Gly Asp Lys Thr Ile Phe Ser Ser Phe Gly
            100                 105                 110

GAA TAT GCT AAA TTT TAT AGT CCA AAA ACT TGT CCA AAC TTC ATA GCA       384
Glu Tyr Ala Lys Phe Tyr Ser Pro Lys Thr Cys Pro Asn Phe Ile Ala
        115                 120                 125

CAA CAG AAA ATA GCA GTA AGA GAC TTG TTA ACA AAA AGT GCA AAA GAT       432
Gln Gln Lys Ile Ala Val Arg Asp Leu Leu Thr Lys Ser Ala Lys Asp
    130                 135                 140

TAT AAA AAT TCA CTT GCA AAA TTA AAA GAA GCG TAT AAA ATA GAT GCG       480
Tyr Lys Asn Ser Leu Ala Lys Leu Lys Glu Ala Tyr Lys Ile Asp Ala
145                 150                 155                 160

ACG ACA AGC CCT CAG AAT GTT TGG CTG GCA TAT GAA ACT TTG AAT TTA       528
Thr Thr Ser Pro Gln Asn Val Trp Leu Ala Tyr Glu Thr Leu Asn Leu
                165                 170                 175

CAA AGC AAG CAA AAT AAC GCT CCA ACA TGG TGG AAT ACT GTA AAC AAA       576
Gln Ser Lys Gln Asn Asn Ala Pro Thr Trp Trp Asn Thr Val Asn Lys
            180                 185                 190

GAT CTA AAA CAA TTC TCT GAG AAA TAT TTA TGG ACC GCC TTG ACT TCT       624
Asp Leu Lys Gln Phe Ser Glu Lys Tyr Leu Trp Thr Ala Leu Thr Ser
        195                 200                 205

AAT GAT AAT CTT AGA AAG ATG TCA GGA GGT CGT ATG ATT AAC GAT ATA       672
Asn Asp Asn Leu Arg Lys Met Ser Gly Gly Arg Met Ile Asn Asp Ile
    210                 215                 220

TTG AAC GAT ATC GAA AAC ATA AAG AAA GGA GAG GGA CAA CCG GGT GCT       720
Leu Asn Asp Ile Glu Asn Ile Lys Lys Gly Glu Gly Gln Pro Gly Ala
225                 230                 235                 240

CCA GGA GGA AAG GAA AAC AAA TTA TCA GTG CTG ACC GTT CCT CAA GCT       768
Pro Gly Gly Lys Glu Asn Lys Leu Ser Val Leu Thr Val Pro Gln Ala
                245                 250                 255

ATC TTA GCA GCA TTT GTT TCA GCA TTT GCT CCC GAA GGT ACA AAA ATT       816
Ile Leu Ala Ala Phe Val Ser Ala Phe Ala Pro Glu Gly Thr Lys Ile
            260                 265                 270

GAA AAT AAG GAC CTT GAT CCG TCT ACT TTA TAT CCT GGC CAA GGA GCA       864
Glu Asn Lys Asp Leu Asp Pro Ser Thr Leu Tyr Pro Gly Gln Gly Ala
        275                 280                 285

CTT CAC GTT ATT GAA CTA CAC CAA GAT AAG AGC GAT TGG AGC ATA AAA       912
Leu His Val Ile Glu Leu His Gln Asp Lys Ser Asp Trp Ser Ile Lys
    290                 295                 300

GTT CTC TAT AGA AAC AAT GAC CAA ATG AAG CTG AAA CCA ATG AAA CTT       960
Val Leu Tyr Arg Asn Asn Asp Gln Met Lys Leu Lys Pro Met Lys Leu
305                 310                 315                 320
```

```
GCA CAA TGC GGT GAC AAG TGT TCT TAT GGT ACT TTC AAA TCA ATG CTA      1008
Ala Gln Cys Gly Asp Lys Cys Ser Tyr Gly Thr Phe Lys Ser Met Leu
                325                 330                 335

CAA AAA TAT AAC ATG GAG AAG GAA GCT CAT GAT AAA TTA TGT AAA ACG      1056
Gln Lys Tyr Asn Met Glu Lys Glu Ala His Asp Lys Leu Cys Lys Thr
            340                 345                 350

TCG                                                                  1059
Ser
```

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 353 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```
Glu Leu Lys Phe Val Phe Ala Thr Ala Arg Gly Met Ser His Thr Pro
  1               5                  10                  15

Cys Asp Tyr Pro Gly Gly Pro Lys Ile Thr His Lys Ser Glu Asp Ser
             20                  25                  30

Ser Gln Leu Thr Pro Ala Gly Gln Glu Glu Ala Leu Lys Ile Gly Lys
         35                  40                  45

Leu Leu Ser Glu His Tyr Arg Thr Asn Leu Lys Val Asp Lys Trp Asp
     50                  55                  60

Ser Asn Lys Asn Tyr Trp Thr Leu Ala Ser Ala Thr Arg Arg Ser Gln
 65                  70                  75                  80

Glu Gly Ala Leu Ile Ile Gly Ser Gly Leu Glu Glu Lys Glu Lys Ala
                 85                  90                  95

Val Trp Thr Lys Glu Lys Gly Asp Lys Thr Ile Phe Ser Ser Phe Gly
            100                 105                 110

Glu Tyr Ala Lys Phe Tyr Ser Pro Lys Thr Cys Pro Asn Phe Ile Ala
        115                 120                 125

Gln Gln Lys Ile Ala Val Arg Asp Leu Leu Thr Lys Ser Ala Lys Asp
    130                 135                 140

Tyr Lys Asn Ser Leu Ala Lys Leu Lys Glu Ala Tyr Lys Ile Asp Ala
145                 150                 155                 160

Thr Thr Ser Pro Gln Asn Val Trp Leu Ala Tyr Glu Thr Leu Asn Leu
                165                 170                 175

Gln Ser Lys Gln Asn Asn Ala Pro Thr Trp Trp Asn Thr Val Asn Lys
            180                 185                 190
```

```
Asp Leu Lys Gln Phe Ser Glu Lys Tyr Leu Trp Thr Ala Leu Thr Ser
        195                 200                 205

Asn Asp Asn Leu Arg Lys Met Ser Gly Gly Arg Met Ile Asn Asp Ile
    210                 215                 220

Leu Asn Asp Ile Glu Asn Ile Lys Lys Gly Glu Gly Gln Pro Gly Ala
225                 230                 235                 240

Pro Gly Gly Lys Glu Asn Lys Leu Ser Val Leu Thr Val Pro Gln Ala
                245                 250                 255

Ile Leu Ala Ala Phe Val Ser Ala Phe Ala Pro Glu Gly Thr Lys Ile
            260                 265                 270

Glu Asn Lys Asp Leu Asp Pro Ser Thr Leu Tyr Pro Gly Gln Gly Ala
        275                 280                 285

Leu His Val Ile Glu Leu His Gln Asp Lys Ser Asp Trp Ser Ile Lys
    290                 295                 300

Val Leu Tyr Arg Asn Asn Asp Gln Met Lys Leu Lys Pro Met Lys Leu
305                 310                 315                 320

Ala Gln Cys Gly Asp Lys Cys Ser Tyr Gly Thr Phe Lys Ser Met Leu
                325                 330                 335

Gln Lys Tyr Asn Met Glu Lys Glu Ala His Asp Lys Leu Cys Lys Thr
            340                 345                 350

Ser
```

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1059 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```
CGACGTTTTA CATAATTTAT CATGAGCTTC CTTCTCCATG TTATATTTTT GTAGCATTGA      60

TTTGAAAGTA CCATAAGAAC ACTTGTCACC GCATTGTGCA AGTTTCATTG GTTTCAGCTT     120

CATTTGGTCA TTGTTTCTAT AGAGAACTTT TATGCTCCAA TCGCTCTTAT CTTGGTGTAG     180

TTCAATAACG TGAAGTGCTC CTTGGCCAGG ATATAAAGTA GACGGATCAA GGTCCTTATT     240

TTCAATTTTT GTACCTTCGG GAGCAAATGC TGAAACAAAT GCTGCTAAGA TAGCTTGAGG     300
```

AACGGTCAGC ACTGATAATT TGTTTTCCTT TCCTCCTGGA GCACCCGGTT GTCCCTCTCC 360

TTTCTTTATG TTTTCGATAT CGTTCAATAT ATCGTTAATC ATACGACCTC CTGACATCTT 420

TCTAAGATTA TCATTAGAAG TCAAGGCGGT CCATAAATAT TTCTCAGAGA ATTGTTTTAG 480

ATCTTTGTTT ACAGTATTCC ACCATGTTGG AGCGTTATTT TGCTTGCTTT GTAAATTCAA 540

AGTTTCATAT GCCAGCCAAA CATTCTGAGG GCTTGTCGTC GCATCTATTT TATACGCTTC 600

TTTTAATTTT GCAAGTGAAT TTTTATAATC TTTTGCACTT TTTGTTAACA AGTCTCTTAC 660

TGCTATTTTC TGTTGTGCTA TGAAGTTTGG ACAAGTTTTT GGACTATAAA ATTTAGCATA 720

TTCACCAAAC GAAGAAAATA TGGTTTTATC TCCTTTCTCT TTTGTCCAAA CTGCCTTTTC 780

CTTTTCTTCT AGACCAGAAC CAATGATAAG CGCTCCTTCT TGAGATCTTC TCGTAGCACT 840

AGCTAATGTC CAATAATTTT TATTTGAATC CCATTTGTCA ACTTTTAAAT TAGTTCTGTA 900

ATGTTCGGAT AATAATTTGC CAATTTTTAA TGCCTCTTCT TGACCTGCCG GTGTCAATTG 960

GCTTGAATCT TCAGACTTGT GTGTAATTTT TGGACCGCCT GGATAATCAC AAGGTGTATG 1020

TGACATACCT CGTGCAGTCG CAAACACAAA TTTCAATTC 1059

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Xaa Glu Leu Lys Phe Val Phe Val Met Val Lys Gly Pro Asp His Glu
1 5 10 15

Ala Cys Asn Tyr Ala Gly Gly Xaa Gln
20 25

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 406 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

```
ATG GTT AAA GGT CCA GAT CAC GAA GCT TGT AAC TAT GCA GGA GGT CCT        48
Met Val Lys Gly Pro Asp His Glu Ala Cys Asn Tyr Ala Gly Gly Pro
  1               5                  10                  15

CAG TTA ACT ACT CTT CAA GAA AAA GAT AGT GTT CTA ACT GAA GAT GGC        96
Gln Leu Thr Thr Leu Gln Glu Lys Asp Ser Val Leu Thr Glu Asp Gly
             20                  25                  30

AAG ACA GAA GCA TAC GAA TTG GGA AAA CTT TTG GAC AAG GTA TAT AAA       144
Lys Thr Glu Ala Tyr Glu Leu Gly Lys Leu Leu Asp Lys Val Tyr Lys
         35                  40                  45

AAA CAA TTA AAA GTT GAC AAA TGG GAT GCC ACG AAA ACC TAC TGG GCT       192
Lys Gln Leu Lys Val Asp Lys Trp Asp Ala Thr Lys Thr Tyr Trp Ala
     50                  55                  60

GTG TCC ACA AAA GCT ATG CGT ACT AAA GAA GCA GCC TTA ATT GTA GGA       240
Val Ser Thr Lys Ala Met Arg Thr Lys Glu Ala Ala Leu Ile Val Gly
 65                  70                  75                  80

GCA GGA TTG GAA AAT AAT CCT GCA AAA GCT AAA GGT AAT TGG ACA CAA       288
Ala Gly Leu Glu Asn Asn Pro Ala Lys Ala Lys Gly Asn Trp Thr Gln
                 85                  90                  95

CAA CAG CTC GAT TCA ACA CAT TTT GAT GCG ATG CCT GGC TTT TCT AGA       336
Gln Gln Leu Asp Ser Thr His Phe Asp Ala Met Pro Gly Phe Ser Arg
            100                 105                 110

TTT TGG AAT CCT CAA CAA TGT CCG GCA TAT TTC AGA GCG CTC TCG CTA       384
Phe Trp Asn Pro Gln Gln Cys Pro Ala Tyr Phe Arg Ala Leu Ser Leu
        115                 120                 125

CAA AAT CAG AAA ATA AAG AAA T                                        406
Gln Asn Gln Lys Ile Lys Lys
    130                 135
```

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```
Met Val Lys Gly Pro Asp His Glu Ala Cys Asn Tyr Ala Gly Gly Pro
```

```
  1               5                  10                  15

Gln Leu Thr Thr Leu Gln Glu Lys Asp Ser Val Leu Thr Glu Asp Gly
            20                  25                  30

Lys Thr Glu Ala Tyr Glu Leu Gly Lys Leu Leu Asp Lys Val Tyr Lys
        35                  40                  45

Lys Gln Leu Lys Val Asp Lys Trp Asp Ala Thr Lys Thr Tyr Trp Ala
    50                  55                  60

Val Ser Thr Lys Ala Met Arg Thr Lys Glu Ala Ala Leu Ile Val Gly
65                  70                  75                  80

Ala Gly Leu Glu Asn Asn Pro Ala Lys Ala Lys Gly Asn Trp Thr Gln
                85                  90                  95

Gln Gln Leu Asp Ser Thr His Phe Asp Ala Met Pro Gly Phe Ser Arg
            100                 105                 110

Phe Trp Asn Pro Gln Gln Cys Pro Ala Tyr Phe Arg Ala Leu Ser Leu
        115                 120                 125

Gln Asn Gln Lys Ile Lys Lys
    130                 135
```

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 407 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

```
AATTTCTTTA TTTTCTGATT TTGTAGCGAG AGCGCTCTGA AATATGCCGG ACATTGTTGA      60

GGATTCCAAA ATCTAGAAAA GCCAGGCATC GCATCAAAAT GTGTTGAATC GAGCTGTTGT     120

TGTGTCCAAT TACCTTTAGC TTTTGCAGGA TTATTTTCCA ATCCTGCTCC TACAATTAAG     180

GCTGCTTCTT TAGTACGCAT AGCTTTTGTG GACACAGCCC AGTAGGTTTT CGTGGCATCC     240

CATTTGTCAA CTTTTAATTG TTTTTTATAT ACCTTGTCCA AAAGTTTTCC CAATTCGTAT     300

GCTTCTGTCT TGCCATCTTC AGTTAGAACA CTATCTTTTT CTTGAAGAGT AGTTAACTGA     360

GGACCTCCTG CATAGTTACA AGCTTCGTGA TCTGGACCTT TAACCAT                   407
```

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 420 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```
GAA GTT ATG GAT AAA TTG CGA AAA CAG GCA CCT CCT AAA ACT GAT GGC        48
Glu Val Met Asp Lys Leu Arg Lys Gln Ala Pro Pro Lys Thr Asp Gly
  1               5                  10                  15

AAT CCT CCA AAA ACA ACC ATA ATG AGT ACA CTT CAA AAG CAA CAA ATA        96
Asn Pro Pro Lys Thr Thr Ile Met Ser Thr Leu Gln Lys Gln Gln Ile
             20                  25                  30

AGT TGC ACA GAA GTG AAA GCG GTT AAC TTA GAA AGT CAT GTT TGT GCT       144
Ser Cys Thr Glu Val Lys Ala Val Asn Leu Glu Ser His Val Cys Ala
         35                  40                  45

TAT GAT TGT AGT CAA CCT GAA ACT GCA GGA ATT ACA TGC AAA GGA AAT       192
Tyr Asp Cys Ser Gln Pro Glu Thr Ala Gly Ile Thr Cys Lys Gly Asn
     50                  55                  60

AAG TGT GAT TGT CCT AAA AAA CGC TAAAAATTTA TTCAAAACAT TTACATTTTT      246
Lys Cys Asp Cys Pro Lys Lys Arg
 65                  70

TATTAATATT CAACTATCAA AAATTCTGTG TTGATTGTTA TTATATTTAT CATAGTTACT     306

AGAAATAAAA TTTTATAACA TTGTTAATTC GAAATTGAAT ACACATAATA TTATAATTAG     366

TGAGGTTAAA AGAAATAAAC CGAATATCCA AATCAAAAAA AAAAAAAAAA AAAA           420
```

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

```
Glu Val Met Asp Lys Leu Arg Lys Gln Ala Pro Pro Lys Thr Asp Gly
  1               5                  10                  15

Asn Pro Pro Lys Thr Thr Ile Met Ser Thr Leu Gln Lys Gln Gln Ile
             20                  25                  30

Ser Cys Thr Glu Val Lys Ala Val Asn Leu Glu Ser His Val Cys Ala
         35                  40                  45
```

```
Tyr Asp Cys Ser Gln Pro Glu Thr Ala Gly Ile Thr Cys Lys Gly Asn
     50                  55                  60

Lys Cys Asp Cys Pro Lys Lys Arg
 65                  70
```

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 420 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```
TTTTTTTTTT TTTTTTTTTT GATTTGGATA TTCGGTTTAT TTCTTTTAAC CTCACTAATT      60

ATAATATTAT GTGTATTCAA TTTCGAATTA ACAATGTTAT AAAATTTTAT TTCTAGTAAC     120

TATGATAAAT ATAATAACAA TCAACACAGA ATTTTTGATA GTTGAATATT AATAAAAAAT     180

GTAAATGTTT TGAATAAATT TTTAGCGTTT TTTAGGACAA TCACACTTAT TTCCTTTGCA     240

TGTAATTCCT GCAGTTTCAG GTTGACTACA ATCATAAGCA CAAACATGAC TTTCTAAGTT     300

AACCGCTTTC ACTTCTGTGC AACTTATTTG TTGCTTTTGA AGTGTACTCA TTATGGTTGT     360

TTTTGGAGGA TTGCCATCAG TTTTAGGAGG TGCCTGTTTT CGCAATTTAT CCATAACTTC     420
```

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

```
Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn Asn Pro Ser
1               5                  10                  15

Thr Lys Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile Glu Asp Phe
            20                  25                  30

Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Cys Lys Ser Gln Cys
        35                  40                  45

Gly Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr Arg Pro Asn
    50                  55                  60
```

Gln Lys His Cys Tyr Cys Glu
65 70

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Asn Asp Lys Leu Gln Phe Val Phe Val Met Ala Arg Gly Pro Asp His
1 5 10 15

Glu Ala Cys Asn Tyr Pro Gly Gly Pro
20 25

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..26
(D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AGTGGATCCG TCAAAAATGG TCACTG 26

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..28
(D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

CCGGAATTCG GTTATTCGCA ATAACAGT 28

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..54
(D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GCGCGGATCC GCATATGGAA GACATCTGGA AGTTAATAA AAAATGTACA TCAG 54

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..45
(D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CCGGAATTCT TATTTATTTT TTGGTCGACA ATAACAAAAG TTTCC 45

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..46
(D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

AAATTTGTAT TTTGTATATG GTATAAAGGA TCCATGATCA TGAAGC 46

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..37
(D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CATGAACCAT GGATAATACA TCGATAAAGA TACTACG 37

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..17
(D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GTAAAACGAC GGCCAGT 17

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..31
(D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GAAGTATATG GACTAAATTA GAGAGCAAGG C 31

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Tyr Phe Asn Lys Leu Val Gln Ser Trp Thr Glu Pro Met Val Phe Lys
1 5 10 15

Tyr Pro Tyr

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..24
(D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GTAATACGAC TCACTATATA GGGC 24